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54 **Novel hybrid transforming growth factors.**

57 The invention relates to novel hybrid TGF- $\beta$ s, a process for the production of biologically active, dimeric hybrid proteins and pharmaceutical compositions comprising them. Hybrid TGF- $\beta$ s produced by this process can be used in various therapeutic modalities such as for the promotion and acceleration of wound healing and bone and tissue repair, the treatment of cancer, as a bone marrow protective agent, mediator of cardioprotection, anti inflammatory or immunosuppressive agent or as a growth regulator in mammalian cell cultures.

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Novel hybrid Transforming Growth Factors

The invention relates to novel recombinant hybrid TGF- $\beta$ s, a process for the production of the recombinant proteins and a process for the preparation of biologically active, dimeric hybrid proteins and pharmaceutical compositions comprising them.

Background of the invention.

TGF- $\beta$  was originally purified to homogeneity from human platelets, human placenta and bovine kidney and identified as a homodimeric protein with a molecular mass of 25.000 D. First characterized by its ability to act synergistically with EGF or TGF- $\alpha$  to induce anchorage-independent growth of untransformed NRK cells; recently, TGF- $\beta$  has been shown to exhibit numerous regulatory effects on a wide variety of both normal and neoplastic cells indicating the importance of this protein as a multifunctional regulator of cellular activity. TGF- $\beta$  may either stimulate mitogenesis, cell proliferation and growth, or may effectively inhibit said processes, or may exhibit other actions like e.g. control of adipogenesis, myogenesis, chondrogenesis, osteogenesis and immune cell function, stimulation of chemotaxis, or induction or inhibition of differentiation depending upon the cell or tissue type, and the presence or absence of other growth factors. Many of the actions of TGF- $\beta$  are related to the response of cells or tissues to stress or injury, and to the repair of resultant damage. After inflammation, TGF- $\beta$  plays the major role in the formation of granulation tissue, increases the expression of genes associated with extracellular matrix formation such as fibronectin, collagen and several protease inhibitors and stimulates collagen-matrix contraction by fibroblasts, suggesting its possible role in connective tissue contraction.

There are five known distinct isoforms of TGF- $\beta$  with 64-82% identity. Until now, three distinct types of TGF- $\beta$ s designated as TGF- $\beta$ 1, TGF- $\beta$ 2 and TGF- $\beta$ 3 thus far have been demonstrated to be expressed in mammalian tissues, TGF- $\beta$ 4 has been described only in chicken and TGF- $\beta$ 5 only in frog. TGF- $\beta$ 1, TGF- $\beta$ 2 and TGF- $\beta$ 3 have been cloned and characterized by sequence analysis. They are synthesized as 390 to 412 amino acids long inactive precursors consisting of a signal sequence, of the Latency Associated Protein LAP and the 112 amino acids long TGF- $\beta$  sequence. In their mature, biologically active forms, TGF- $\beta$ s are acid- and heat-stable disulfide-linked homodimers of two polypeptide chains of 112 amino acids each.

The complete amino acid sequences of human, murine and simian TGF- $\beta$ 1 show remarkable sequence conservation, differing only in a single amino acid residue. Comparison of the amino acid sequence of human TGF- $\beta$ 1, human TGF- $\beta$ 2 and human TGF- $\beta$ 3 has demonstrated that the three proteins exhibit in their mature forms about 70-80 % sequence identity. A heterodimeric TGF- $\beta$ 1.2 has been isolated from porcine platelets and consists of one subunit of TGF- $\beta$ 1 disulfide-linked to one subunit of TGF- $\beta$ 2.

Natural sources (e.g. platelets) are inadequate to supply the amounts required for clinical studies and expected therapeutic usage. Therefore, attempts have recently been undertaken aiming to produce TGF- $\beta$ s by means of recombinant techniques. However, it has proven to be extremely difficult to synthesize recombinant TGF- $\beta$  while retaining its biological activity. TGF- $\beta$ 1, TGF- $\beta$ 2 and TGF- $\beta$ 3 contain 9 cysteine residues each, at least some of which are involved in intrachain and interchain disulfide bond formation which results in the complex tertiary structure of the biologically active, dimeric molecules. Heterologous expression of TGF- $\beta$  may lead to a product which, although having the correct primary structure, fails to fold properly to produce the correct secondary or tertiary structures and which, therefore, lacks the biological activity. To date, the secondary and tertiary structures of TGF- $\beta$ s are unknown.

Taking the complexity of the native TGF- $\beta$  molecules into account, it has generally been considered expedient to express the respective TGF- $\beta$  genes in cells derived from higher organisms.

However, following expression of full-length DNAs encoding the precursor forms of TGF- $\beta$ s (390-414aa) in eukaryotic systems, yields of biologically active, correctly folded material remain far from satisfactory. Only low levels of expression have been described for TGF- $\beta$ 1, TGF- $\beta$ 2 and TGF- $\beta$ 3 in CHO cells amplified with Methotrexate (MTX), e.g. expression of 6  $\mu$ g/ml TGF- $\beta$ 1 at 20  $\mu$ M MTX concentration (Gentry, L. E. et al., (1987) *Molec. Cell. Biol.* 7:3418-3427), expression of 5  $\mu$ g/ml TGF- $\beta$ 2 at 10  $\mu$ M and 50  $\mu$ M MTX concentration (Madisen, L. et al., (1990) *Growth Factors* 3:129-138), expression of 2  $\mu$ g/ml TGF- $\beta$ 3 at 1.6mM MTX concentration (Graycar, J.L. et al., (1989) *Mol. Endocrinol.* 3:1977-1986) and 30 ng/ml at 20mM MTX concentration (Ten Dijke, P. et al., (1990) *Annals of the New York Academy of Sciences* 593:26-42). In all 3 cases the TGF- $\beta$  is secreted in a latent form since acidification is necessary for detection of biological activity.

EP-A-0 433 225 describes a microbial-based process for the production of biologically active, dimeric TGF- $\beta$ -like protein from its denatured or otherwise non-native form. Considerable amounts of TGF- $\beta$  can be obtained when the monomeric form is subjected to refolding.

Different TGF- $\beta$  isoforms have different potencies and/or activities in various systems. For example,

- TGF- $\beta$ 3 is 10-fold more active than TGF- $\beta$ 2 in inducing mesoderm formation in *Xenopus laevis*. TGF- $\beta$ 1 is inactive in this assay.
- TGF- $\beta$ 1 is 10 to 100-fold more potent than TGF- $\beta$ 2 in inhibiting DNA synthesis in bovine aortic endothelial cells.
- TGF- $\beta$ 2 and TGF- $\beta$ 3 are markedly more potent than TGF- $\beta$ 1 in stimulating proliferation of AKR-2B fibroblasts and in inhibiting DNA-synthesis in CCL64 Mink Lung Epithelial cells. TGF- $\beta$ 1 is markedly more potent than TGF- $\beta$ 2 or -3 in inhibiting the proliferation of the mammary carcinoma cell line MCF-7. TGF- $\beta$ 3 is markedly more potent than TGF- $\beta$ 1 or -2 in inhibiting DNA synthesis in mouse and human keratinocytes.
- TGF- $\beta$ 2 is markedly more active in vivo, in stimulating bone formation than TGF- $\beta$ 1.

A need exists for hybrid TGF- $\beta$  molecules with altered or mixed activities as compared with the parent molecules which hybrid TGF- $\beta$ s exhibit improved activities and/or novel or advantageous properties in certain biological systems.

#### Object of the invention

It is an object of the present invention to provide novel hybrid TGF- $\beta$  molecules, recombinant DNA molecules encoding same, hybrid vectors comprising such recombinant DNA molecules, transformed hosts suitable for the multiplication and/or expression of the recombinant DNA molecules, and processes for the preparation of the hosts, DNA molecules and hybrid TGF- $\beta$  molecules.

#### Detailed description of the invention

The invention concerns novel hybrid TGF- $\beta$  molecules, preferentially such having biological TGF- $\beta$  activity. "Biological activity" for the purpose herein is defined as either

- (a) the cell migration promoting activity on normal Balb/c 3T3 fibroblasts, which can be measured by counting the number of cells that migrate into a "wounded" mono-layer culture of said cells, in the presence of a serum-free medium containing the TGF- $\beta$ -like protein, as compared to the number of cells that migrate in the absence of the TGF- $\beta$ -like protein, or
- (b) the growth promoting activity on normal Balb/c 3T3 fibroblasts determined by the stimulatory effect of the TGF- $\beta$ -like protein on cellular DNA synthesis and cell division, or
- (c) the growth inhibition of A375 melanoma cells determined by a colorimetric assay which reflects the number of cells treated with the TGF- $\beta$ -like protein for a given culture period as compared to the number of non-treated cells, or
- (d) the accelerated healing of partial-thickness burn wounds, by a process of re-epithelialization, in old mice following multiple topical applications of the TGF- $\beta$ -like protein as compared to untreated control wounds, or
- (e) the accelerated healing of full-thickness incisional wounds, as determined by tensile strength measurements and the histological analyses of biopsies, in adult rats following single topical applications of the TGF- $\beta$ -like protein as compared to untreated control wounds, or
- (f) the increase in formation of fibrous granulation tissue, together with a marked increase in vascularity of the said tissue, both in and around porous wound-chamber implants in adult rats following multiple local injections of the TGF- $\beta$ -like protein into the chamber as compared to untreated control chambers.

A substantial feature of the said novel hybrid TGF- $\beta$  molecules is that they consist of two or more, preferentially of 2, 3, 4, 5 or 6, more preferably of two parts, the said parts consisting of contiguous stretches of 6 or more amino acids of a sequence which occurs in the mature part in two or more, preferentially in two or three, more preferably in two, of the TGF- $\beta$  isoforms defined hereinafter. In all cases the stretches of amino acid residues in the hybrid molecules correspond to contiguous stretches of an equal length which occur at the corresponding locations in the primary amino acid sequence of a different TGF- $\beta$  isoform.

The term "TGF- $\beta$ -isoform" is intended to embrace TGF- $\beta$ 1, TGF- $\beta$ 2 and TGF- $\beta$ 3 of mammalian such as human or animal origin, e.g. simian, murine, porcine, equine or bovine, and TGF- $\beta$ 4 of chicken and TGF- $\beta$ 5 of frog. It preferentially includes TGF- $\beta$ 1, TGF- $\beta$ 2, and TGF- $\beta$ 3, most preferentially human TGF- $\beta$ 1, human TGF- $\beta$ 2 and human TGF- $\beta$ 3 with the amino acid sequences depicted the Sequence Listing under SEQ ID NO. 1 to 3.

The preferred type of hybrid proteins of the invention comprises two parts, each consisting of contiguous amino acid stretches from different TGF- $\beta$  isoforms. More preferred hybrid TGF- $\beta$  molecules are those consisting of a N-terminal part of TGF- $\beta$ 1 and a C-terminal part of TGF- $\beta$ 2, a N-terminal part of TGF- $\beta$ 2 and a C-terminal part of TGF- $\beta$ 1, a N-terminal part of TGF- $\beta$ 1 and a C-terminal part of TGF- $\beta$ 3, a N-terminal part of

TGF- $\beta$ 3 and a C-terminal part of TGF- $\beta$ 1, a N-terminal part of TGF- $\beta$ 2 and a C-terminal part of TGF- $\beta$ 3, or a N-terminal part of TGF- $\beta$ 3 and a C-terminal part of TGF- $\beta$ 2. Most preferably, these hybrid TGF- $\beta$  molecules are composed of parts of TGF- $\beta$ 1, TGF- $\beta$ 2 and/or TGF- $\beta$ 3 sequences shown in the Sequence listing under SEQ ID NO. 1 to 3.

5 Preferred hinge point between the amino acid stretches derived from the parent TGF- $\beta$  isoforms are between amino acids 56 and 57, 79 and 80, 90 and 91, 22 and 23, or between 44 and 45 (numbering relates to the amino acids numbers of human TGF- $\beta$ , starting at the N-terminus). Thus, preferred hybrids of the present invention are composed of the 56, 79, 90, 22 or 44 N-terminal amino acids of the TGF- $\beta$  isoform providing the N-terminal part of the hybrid and of the 56, 33, 22, 90, or 68, respectively, C-terminal amino acids of the TGF- $\beta$  isoform providing the C-terminal part of the hybrid molecule.

10 Preferred forms of the hybrid TGF- $\beta$  molecules composed of parts of TGF- $\beta$ 1, TGF- $\beta$ 2 and/or TGF- $\beta$ 3 sequences shown in the Sequence listing under SEQ ID NO. 1 to 3 are hybrid proteins having the hinge points between amino acids 44 and 45 and consisting of the 44 N-terminal amino acids of TGF- $\beta$ 1 and of the 68 C-terminal amino acids of TGF- $\beta$ 2, of the 44 N-terminal amino acids of TGF- $\beta$ 2 and of the 68 C-terminal amino acids of TGF- $\beta$ 1, of the 44 N-terminal amino acids of TGF- $\beta$ 3 and of the 68 C-terminal amino acids of TGF- $\beta$ 1, of the 44 N-terminal amino acids of TGF- $\beta$ 2 and of the 68 C-terminal amino acids of TGF- $\beta$ 3, or even more preferably of the 44 N-terminal amino acids of TGF- $\beta$ 3 and of the 68 C-terminal amino acids of TGF- $\beta$ 2. These hybrids are named TGF- $\beta$ 1(44/45) $\beta$ 2, TGF- $\beta$ 2(44/45) $\beta$ 1, TGF- $\beta$ 1(44/45) $\beta$ 3, TGF- $\beta$ 3(44/45) $\beta$ 1, and TGF- $\beta$ 2(44/45) $\beta$ 3, respectively. The even more preferred form is accordingly named TGF- $\beta$ 3(44/45) $\beta$ 2. The amino acid sequences of these hybrids as well as DNA sequences encoding them are depicted in the sequence listing (SEQ ID NOS. 4 to 9).

25 Preferred forms of the hybrid TGF- $\beta$  molecules composed of parts of TGF- $\beta$ 1, TGF- $\beta$ 2 and/or TGF- $\beta$ 3 sequences shown in the Sequence listing under SEQ ID NO. 1 to 3 are also hybrids consisting of the TGF- $\beta$ 1 N-terminal and TGF- $\beta$ 2 C-terminal halves, i.e. the 56 N-terminal amino acids of TGF- $\beta$ 1 and the 56 C-terminal amino acids of TGF- $\beta$ 2, of the TGF- $\beta$ 2 N-terminal and TGF- $\beta$ 1 C-terminal halves, of the TGF- $\beta$ 1 N-terminal and TGF- $\beta$ 3 C-terminal halves, of the TGF- $\beta$ 3 N-terminal and TGF- $\beta$ 1 C-terminal halves, of the TGF- $\beta$ 2 N-terminal and TGF- $\beta$ 3 C-terminal halves, and of the TGF- $\beta$ 3 N-terminal and TGF- $\beta$ 2 C-terminal halves. These hybrids are named TGF- $\beta$ 1(56/57) $\beta$ 2, TGF- $\beta$ 2(56/57) $\beta$ 1, TGF- $\beta$ 1(56/57) $\beta$ 3, TGF- $\beta$ 3(56/57) $\beta$ 1, TGF- $\beta$ 2(56/57) $\beta$ 3, and TGF- $\beta$ 3(56/57) $\beta$ 2, respectively.

30 Likewise, preferred forms of the hybrid TGF- $\beta$  molecules composed of parts of TGF- $\beta$ 1, TGF- $\beta$ 2 and/or TGF- $\beta$ 3 sequences shown in the Sequence listing under SEQ ID NO. 1 to 3 are also hybrids having the hinge point between amino acid 79 and 80. In accordance with the nomenclature explained hereinbefore they are named TGF- $\beta$ 1(79/80) $\beta$ 2, TGF- $\beta$ 2(79/80) $\beta$ 1, TGF- $\beta$ 1(79/80) $\beta$ 3, TGF- $\beta$ 3(79/80) $\beta$ 1, TGF- $\beta$ 3(79/80) $\beta$ 2, and TGF- $\beta$ 2(79/80) $\beta$ 3.

Likewise, preferred forms of the hybrid TGF- $\beta$  molecules composed of parts of TGF- $\beta$ 1, TGF- $\beta$ 2 and/or TGF- $\beta$ 3 sequences shown in the Sequence listing under SEQ ID NO. 1 to 3 are also the hybrids TGF- $\beta$ 1(90/91) $\beta$ 2, TGF- $\beta$ 2(90/91) $\beta$ 1, TGF- $\beta$ 1(90/91) $\beta$ 3, TGF- $\beta$ 3(90/91) $\beta$ 1, TGF- $\beta$ 3(90/91) $\beta$ 2, and TGF- $\beta$ 2(90/91) $\beta$ 3, all having the hinge point between amino acid 90 and 91.

40 Likewise, preferred forms of the hybrid TGF- $\beta$  molecules composed of parts of TGF- $\beta$ 1, TGF- $\beta$ 2 and/or TGF- $\beta$ 3 sequences shown in the Sequence listing under SEQ ID NO. 1 to 3 are also the hybrids TGF- $\beta$ 1(22/23) $\beta$ 2, TGF- $\beta$ 2(22/23) $\beta$ 1, TGF- $\beta$ 1(22/23) $\beta$ 3, TGF- $\beta$ 3(22/23) $\beta$ 1, TGF- $\beta$ 3(22/23) $\beta$ 2, and TGF- $\beta$ 2(22/23) $\beta$ 3, all having the hinge point between amino acid 22 and 23.

45 The amino acid sequences of the preferred hybrids and the nucleotide sequences encoding them can be easily deduced from the amino acid sequences of the parent TGF- $\beta$ 1, - $\beta$ 2, and - $\beta$ 3 molecules and the corresponding DNA sequences given in the sequence listing under SEQ ID NO. 1 to 3.

The invention also concerns recombinant DNA molecules encoding hybrid TGF- $\beta$  molecules of the invention. Preferred DNA molecules are those which are coding for the preferred hybrid proteins.

50 The nucleotide sequences encoding the TGF- $\beta$  isoforms specified above are known from literature or can be deduced from the amino acid sequences of the proteins according to conventional rules. Starting from the nucleotide sequences encoding the parent TGF- $\beta$  isoform molecules, a DNA molecule encoding any desired hybrid molecule can be deduced and constructed according to conventional methods known in the art including, but not limited to, the use of polymerase chain reaction (PCR) technology, DNA restriction enzymes, synthetic oligonucleotides, DNA ligases and DNA amplification techniques. Alternatively, the coding sequences may be synthesized in whole or in part using chemical methods known in the art.

55 The DNA coding for the TGF- $\beta$  isoforms, e.g. for human TGF- $\beta$ 1, -2 and -3, i.e. the parent molecules of preferred hybrids of the invention, may be obtained from human cell sources by conventional methods, e.g. by applying cDNA technology, from vectors available in the art or by chemical synthesis of the DNA.

A recombinant DNA molecule encoding hybrid TGF- $\beta$  molecules of the invention also comprises DNA sequences which are degenerate within the meaning of the genetic code in that an unlimited number of nucleotides are replaced by other nucleotides without changing the amino acid sequence for which they code. Such degenerate DNA sequences may be useful because of the occurrence of different restriction patterns or because of preferred codon usage in a particular host.

The invention also concerns hybrid vectors comprising a DNA sequence encoding a hybrid TGF- $\beta$  molecule of the invention. The hybrid vectors of the invention provide for replication and optionally expression of the DNA encoding a hybrid of the invention, either as an extrachromosomal element or by integration into the host genome. Several possible vector systems are available, and the vector selected is depending on the host cells envisaged for transformation.

A hybrid vector of the invention comprises a DNA sequence encoding a hybrid TGF- $\beta$  molecule of the invention linked with an origin of replication allowing the replication of the vector in the host cell, or a functionally equivalent sequence, e.g. an autonomously replicating sequence ARS from yeast. Another type of vector, i.e. an expression vector, comprises a DNA sequence encoding a hybrid TGF- $\beta$  molecule of the invention operably linked with expression control sequences, e.g. promoters, which ensure the effective expression of the hybrid TGF- $\beta$  proteins in a transformed host, and an origin of replication allowing the replication of the vector in the host cell, or a functionally equivalent sequence. However, in case that the vector of the invention is a so-called integrative vector, i.e. it is integrated into a host chromosome after transformation and is replicated as part of the chromosome, it does not necessarily comprise an origin of replication or functionally equivalent sequence.

Suitable hybrid vectors may be derived from any vector useful in the art of genetic engineering, such as from viruses, phages, cosmids, plasmids or chromosomal DNA. Examples of vectors that are suitable for the expression of the hybrid TGF- $\beta$  protein in an *E. coli* strain are bacteriophages, for example derivatives of the bacteriophage  $\lambda$  or M13 or plasmids, such as the plasmid pBR322 and its derivative pPLMu. Examples of vectors that are suitable for the expression of the hybrid TGF- $\beta$  protein in a yeast strain are  $2\mu$  based plasmids. Vectors suitable for the expression in higher eukaryotic cells are vectors based on the insect Baculovirus or on other viruses, such as SV40, Herpes viruses, Papillomaviruses, Retroviruses and the like. Suitable vectors may contain a marker gene, which renders possible the selection and identification of the microorganisms transformed by the expression plasmids by means of a phenotype feature. Suitable marker genes impart to the microorganism, for example, resistance to heavy metals, antibiotics such as ampicillin or tetracyclin, and the like.

Several promoters can be used for regulating the expression of hybrid TGF- $\beta$  proteins in *E. coli*. Especially promoters of strongly expressed genes are used. Suitable promoters are the *E. coli* lac, tac, trp and lpp promoters, furthermore the phage  $\lambda$ N or the phage  $\lambda$ L promoter, and others.

Vectors suitable for replication and expression in *S. cerevisiae* contain a yeast-replication origin and a selective genetic marker for yeast. Hybrid vectors that contain a yeast replication origin, for example the chromosomal autonomously replicating segment (ars), are retained extrachromosomally within the yeast cell after transformation and are replicated autonomously during mitosis. Also, hybrid vectors that contain sequences homologous to the yeast  $2\mu$  plasmid DNA can be used. Such hybrid vectors are integrated by recombination in  $2\mu$  plasmids already present within the cell, or replicate autonomously. Suitable marker genes for yeast are especially those that impart antibiotic resistance to the host or, in the case of auxotrophic yeast mutants, genes that complement the host lesions. Corresponding genes impart, for example, resistance to the antibiotic cycloheximide or provide for prototrophy in an auxotrophic yeast mutant, for example the URA3, LEU2, HIS3 or the TRP1 gene.

Promoters suitable for expression in yeast are, for example, those of the ADHI, ADHI1, or PHO5 gene, and also promoters involved in glycolysis, for example the PGK or the GAP promoter.

Optionally, signal sequences which allow the secretion of the hybrid TGF- $\beta$  protein can be included in the expression vector. Suitable signal sequences are e.g. derived from the yeast acid phosphatase (PHO5) or the yeast invertase gene.

The present invention also concerns a method for the preparation of the DNA molecules of the invention defined hereinbefore or in the examples. They are prepared according to conventional methods, e.g. by means of restriction enzymes, ligases, phosphatases or polymerases, or by applying polymerase chain reaction (PCR) techniques, or by conventional chemical synthesis, or by isolating the desired DNA molecules from natural sources or transformed hosts, e.g. by a method comprising culturing a host transformed with a vector providing for the replication of the desired DNA molecule and isolating the DNA molecule from the host by conventional methods, e.g. by extraction with phenol and/or chloroform.

Microbial hosts comprising a nucleotide sequence encoding the hybrid TGF- $\beta$  protein linked in the proper reading frame to an expression control sequence can be prepared by recombinant DNA techniques which are well known in the art and which comprise the steps of

- preparing a hybrid vector comprising a DNA sequence encoding the hybrid TGF- $\beta$  protein under the expression control of a suitable expression control sequence,
- transforming said microbial host with said hybrid vector, and
- selecting transformed microbial host cells from untransformed host cells.

5 The selection of a suitable vector is determined by the microbial host cell provided for the transformation. Suitable microbial hosts for performing the present invention are yeast strains as Saccharomyces cerevisiae or bacteria such as Bacillus subtilis or preferentially Escherichia coli.

The transformed microbial hosts are cultured in a liquid medium containing assimilable sources of carbon, nitrogen and inorganic salts, applying methods known in the art.

10 Various carbon sources are usable. Example of preferred carbon sources are assimilable carbohydrates, such as glucose, maltose, mannitol, fructose or lactose, or an acetate such as sodium acetate, which can be used either alone or in suitable mixtures. Suitable nitrogen sources include, for example, amino acids, such as casamino acids, peptides and proteins and their degradation products, such as tryptone, peptone or meat extracts, furthermore yeast extract, malt extract, corn steep liquor, as well as ammonium salts, such as ammonium chloride, sulphate or nitrate which can be used either alone or in suitable mixtures. Inorganic salts which may be used include, for example, sulphates, chlorides, phosphates and carbonates of sodium, potassium, magnesium and calcium. Additionally, the nutrient medium may also contain growth promoting substances. Substances which promote growth include, for example, trace elements, such as iron, zinc, manganese and the like, or individual amino acids.

20 The monomeric form of the TGF- $\beta$ -like protein can be produced by means of recombinant DNA technology or synthetically by methods well-known in the art. The dimeric form is the mature, biologically active molecule consisting of two disulfide-linked polypeptide chains. This dimeric form can either be produced directly in an appropriate expression system well known in the art, e.g. CHO cells, or preferentially by expressing the monomer in a microbial host cell, preferentially in *E. coli*, and subjecting this monomer to refolding.

25 Thus, the invention relates to a process for the production of a dimeric, biologically active hybrid TGF- $\beta$  protein, in which the monomeric form of a hybrid TGF- $\beta$  protein, preferentially one of those hybrids specified hereinbefore, is produced by the steps of:

- (a) culturing a microbial host comprising a nucleotide sequence encoding the hybrid TGF- $\beta$  protein linked in the proper reading frame to an expression control sequence such that said protein is expressed,
- (b) recovering the hybrid TGF- $\beta$  protein in a denatured, monomeric, soluble form.

30 The monomeric hybrid TGF- $\beta$  protein is recovered from the microbial host cells by methods well known in the art. These methods include lysis or mechanical disruption of the cells in order to release the desired protein, followed by the separation of the hybrid TGF- $\beta$  protein from the host cell proteins, e.g. by precipitation and/or chromatographic means.

35 In cases where the monomeric hybrid TGF- $\beta$  protein is produced in the microbial host cells as an insoluble aggregate (inclusion body) it has to be solubilized before being exposed to the refolding conditions. Accordingly, the present invention further relates to a process wherein the monomeric hybrid TGF- $\beta$  protein is produced by the steps of:

- (a) isolating the water-insoluble protein fraction containing the hybrid TGF- $\beta$  protein from the host cells and
- (b) solubilizing the hybrid TGF- $\beta$  protein.

40 Solubilization and denaturation of the monomer is achieved by acidification of the crude protein suspension containing the monomeric hybrid TGF- $\beta$  protein in the non-soluble form to a pH of about 1 to about 4, preferably to about 2.5, optionally in the presence of a reducing agent, such as DTT, or by the addition of chaotropic agents, preferably guanidine HCl or most preferably urea, in a concentration of about 4 to 9 M, basic pH or elevated temperatures as described before. The solubilized monomer can be purified from solubilizing chaotropes by dialysis and, if a precipitate occurs during dialysis, by additional centrifugation. The solubilized monomer is chromatographically purified and used for refolding to get the biologically active, dimeric product.

45 Refolding is performed using a refolding process known in the art (European Patent Application EP-A-0 433 225). In such a refolding process the in vitro refolding of monomeric, denatured TGF- $\beta$  hybrid protein into the biologically active, disulfide-linked, dimeric form is achieved by mixing a solution of monomeric denatured TGF- $\beta$  hybrid protein with a refolding buffer. Refolding buffer consists of a buffering salt, e.g. Tris/HCl, an additional salt, e.g. NaCl, optionally a chelating agent, e.g. EDTA, a sulfhydryl/disulfide redox system, e.g. glutathione in its reduced and oxidized form, respectively, and a solubilizing agent which permits folding of the monomeric TGF- $\beta$  hybrid protein into the spatial conformation which is associated with the biological activity, while retaining said monomer, the folding intermediates and the dimer in solution.

55 Preferred solubilizing agents are the zwitterionic detergents 3-(3-chloramidopropyl)dimethyl-ammonio-1-propanesulfonate [CHAPS] or 3-(3-chloramidopropyl)dimethyl-ammonio-2-hydroxy-1-propanesulfonate [CHAP-

SO], or other detergents with similar solubilizing characteristics. Most preferred is CHAPS.

Preferred pH, temperature and concentrations of the chemicals contained in the refolding buffer are: buffering salt: about 10 mM to about 1 M, most preferably about 100 mM; additional salt: about 10 mM to about 2 M, most preferably about 1 M; chelating agent: about 0.1 to about 100 mM, most preferably about 2 mM; 5 sulfhydryl/disulfide redox agents: about 0.1 to about 10 mM, with a molar ratio between about 100:1 and about 1:100, most preferably about 2.5 mM reduced and about 1 mM oxidized glutathione; solubilizing agent: about 10 to about 100 mM, most preferably about 30 mM; pH: about 7 to about 10, most preferably between about 8 and 9; temperature: about 0 °C and 37 °C, most preferably about 4°C.

After refolding, the biologically active dimer is purified in order to remove impurities, in particular, pyrogens 10 or other endotoxins which might be present in the preparation after production of the recombinant protein in microbial host cells. Separation of the dimer is performed by chromatography such as sizing gel chromatography, hydrophobic interaction chromatography or ion exchange chromatography, e.g. on a Mono S column, and reverse phase HPLC.

The present invention further relates to dimeric biologically active hybrid TGF- $\beta$  proteins when produced 15 according to the process of the invention. These hybrid TGF- $\beta$  proteins can be used in a variety of therapeutic modalities.

The present invention concerns further a pharmaceutical composition comprising an effective amount of a dimeric, biologically active hybrid TGF- $\beta$  protein produced according to the invention, or a pharmaceutically acceptable salt thereof in dosage unit form.

Such composition is in the form of infusion solutions or preparations for parenteral, for example intramuscular or intravenous, oral, or especially for local, i.e. topical, administration, respectively. The solutions are preferably isotonic aqueous solutions or suspensions which can be prepared before use, for example from lyophilised preparations which contain the active ingredient alone or together with a pharmaceutically acceptable carrier. Solutions for parenteral use are usually aqueous solutions. They are prepared in conventional manner 25 and may contain in addition to the active ingredient physiological saline, a stabilizer, such as human serum albumin, amino acids, such as arginine or glycine, and a carbohydrate, such as glucose, mannose, dextran or hydroxyethyl starch. The pH may be adjusted with a buffer, e.g. a phosphate, succinate or an amino acid to about 4.5 to 7. Usually the vials are filled with the solution and lyophilized for longer storage.

The compositions contain conventional adjuncts, for example preservatives, stabilisers, wetting agents 30 and/or emulsifiers, solubilisers, salts for regulating the osmotic pressure and/or buffers. The present pharmaceutical compositions, which may, if desired, contain further pharmacologically valuable substances, are produced in a manner known *per se*, for example by means of conventional mixing, dissolving, lyophilising and/or sterilising processes, and contain from approximately 1 ng to 100  $\mu$ g/g, especially from approximately 10 ng to 10  $\mu$ g/g of preparation, and in the case of lyophilisates up to 100 %, of the active ingredient.

The hybrid TGF- $\beta$  proteins are dual in character in that they on the one hand stimulate the proliferation 35 of certain cell types, namely fibroblasts, and on the other hand inhibit the proliferation of other cell types, namely tumor cells and cells of the immune system.

The dimeric, biologically active hybrid TGF- $\beta$  proteins produced according to the invention, optionally in the form of their salts, such as in particular non-toxic pharmaceutical acid addition salts, optionally in form of 40 pharmaceutical formulations, are applied in an effective amount. By the term "effective amount" is intended an amount which exerts a significant healing, e.g. an amount which stimulates the desired cells to grow and which is not toxic to normal cells. This amount can be determined e.g. by in vitro growth experiments. Due to the dual character of hybrid TGF- $\beta$  proteins, an "effective amount" is also such which to a significant extent inhibits the growth and proliferation of tumour cells and cells of the immune system. If human or veterinary 45 use is intended, the amount has to be adjusted to the particular tissue to be treated, the mode of application, the severity of the disease, and the age and general condition of the patient to be treated. In general, the either single or daily dosages for adult humans will be in the range of about 0.01 to 20  $\mu$ g for both the growth stimulating and the inhibiting effect.

The pharmaceutical composition of this invention have a clinical use in the treatment of animals, particularly mammals, more particularly human beings, and, in the case of wound healing, most particularly of old 50 human beings.

The compositions of this invention promote cell migration and proliferation. Since wound healing involves both cell migration and cell proliferation patterns these in vitro findings become directly relevant to the in vivo wound healing process.

55 Prevention or treatment of bed sores (decubitus ulcers) is a preferred use since they frequently occur in hospital patients, particularly geriatric and wheel chair patients. In elderly people the wound healing process is slower and this group of patients tends to show a higher incidence of wounds (not only decubitus and diabetic ulcers, but trauma, burns and the like) that either heal slowly or do not heal at all.

Two types of application of the compositions of this invention are proposed for both veterinary and, in particular, human medicine.

The first, and preferred application is a topical one for the promotion of surface wound healing, particularly in elderly human beings where the wound healing processes are noticeably slower. There are no limitations as to the type of wound that may be treated, and these include (but are not limited to): Surface ulcers including decubital (bed sore), diabetic, dental, oral, varicose and haemophilic surface ulcers; burns (especially second and third degree); surgical incisions (including those of dental and cosmetic surgery); accidental wounds (including incisions, penetrations, lacerations and other traumata) and therapeutically induced wounds (including those induced during radiotherapy). When applied topically, the compositions may be combined with other ingredients, such as adjuvants, carriers, solubilizing agents and any other known, or as yet unknown, secondary growth factor(s). There are no limitations as to the nature of these ingredients except that they must be pharmaceutically and physiologically acceptable for administration and must not degrade the activity, or render harmfully toxic, the active ingredients of the compositions. When the compositions of this invention are applied to surface ulcers, burns, surgical or accidental wounds, the compositions are preferably in the form of a powder, gel, ointment, salve or irrigant, or they may be impregnated into transdermal patches, plasters and bandages, preferably in a liquid or semi-liquid form, or they may be incorporated into a tooth paste or a gum or resin for chewing.

The second application is a systemic one for the healing of internal wounds either following surgery, or damage to the tissues of the inner organs where surgery is either impossible or is not required. Again, there are no limitations as to the type of tissue or wound to be treated and these include (but are not limited to) deep surgical incisions to the inner organs and tissues; bone and cartilage (after fracture); gastric, duodenal and other intestinal ulcers. When applied systemically, the compositions of the invention may be formulated as liquids, pills, tablets, lozenges for enteral administration, or in liquid form for parenteral injection. For the treatment of internal incisions following surgery, they may be in the form of an irrigant, preferably in combination with a physiologically acceptable saline solution. Again, the active ingredients of the compositions may be combined with other ingredients such as adjuvants, carriers, solubilizing agents and any other known, or as yet unknown, secondary growth factor(s). There are no limitations as to the nature of these ingredients except that they must be pharmaceutically and physiologically acceptable for administration and must not degrade the activity, or render harmfully toxic, the active ingredients of these compositions.

For healing the wounds, the amount of active ingredient to be applied has to be adjusted to the type, severity and location of the wound, and also to the age and general condition of the patient to be treated. In general a single or daily amount of from about 0.1  $\mu$ g to 20  $\mu$ g of hybrid TGF- $\beta$  protein per 1 cm<sup>2</sup> of wound has already a significant healing effect. For internal use a higher amount should be applied depending on the mode of administration due to the dilution of the hybrid TGF- $\beta$  protein in the body fluids.

Further uses of the hybrid TGF- $\beta$  proteins produced according to the invention are in bone and tissue repair, treatment of cancer in mammals, as an anti-inflammatory or immuno-suppressive agent, as a growth regulator in mammalian cell cultures or as a bone marrow protective agent or mediator of cardioprotection.

The most preferred embodiments of the present invention are those described hereinafter in the Examples.

The following Examples are illustrating the present invention, however, are in no way intended to limit it.

### Examples

#### Example 1: Construction of hybrid TGF- $\beta$ cDNAs

The sequences of the TGF- $\beta$ 1, TGF- $\beta$ 2 and TGF- $\beta$ 3 cDNA referred to hereinafter is depicted in the Sequence listing under SEQ ID NO. 1 to 3.

The various oligomers used for construction of the hybrid cDNAs are synthesized on an Applied Biosystems DNA Synthesizer and are all depicted in the Sequence listing.

Using Polymerase Chain Reaction (PCR) technique TGF- $\beta$ 1, TGF- $\beta$ 2 and TGF- $\beta$ 3 cDNA fragments are firstly amplified and then joined together in various twin combinations to produce the corresponding TGF- $\beta$ 1(44/45) $\beta$ 2, TGF- $\beta$ 2(44/45) $\beta$ 1, TGF- $\beta$ 1(44/45) $\beta$ 3, TGF- $\beta$ 3(44/45) $\beta$ 1, TGF- $\beta$ 2(44/45) $\beta$ 3 and TGF- $\beta$ 3(44/45) $\beta$ 2 hybrid cDNAs (see SEQ ID NO. 4 to 9) as well as TGF- $\beta$ 1(56/57) $\beta$ 2, TGF- $\beta$ 2(56/57) $\beta$ 1, TGF- $\beta$ 1(56/57) $\beta$ 3, TGF- $\beta$ 3(56/57) $\beta$ 1, TGF- $\beta$ 2(56/57) $\beta$ 3, TGF- $\beta$ 3(56/57) $\beta$ 2, TGF- $\beta$ 1(79/80) $\beta$ 2, TGF- $\beta$ 2(79/80) $\beta$ 1, TGF- $\beta$ 1(79/80) $\beta$ 3, TGF- $\beta$ 3(79/80) $\beta$ 1, TGF- $\beta$ 2(79/80) $\beta$ 3, TGF- $\beta$ 3(79/80) $\beta$ 2, TGF- $\beta$ 1(90/91) $\beta$ 2, TGF- $\beta$ 2(90/91) $\beta$ 1, TGF- $\beta$ 1(90/91) $\beta$ 3, TGF- $\beta$ 3(90/91) $\beta$ 1, TGF- $\beta$ 2(90/91) $\beta$ 3, TGF- $\beta$ 3(90/91) $\beta$ 2, TGF- $\beta$ 1(22/23) $\beta$ 2, TGF- $\beta$ 2(22/23) $\beta$ 1, TGF- $\beta$ 1(22/23) $\beta$ 3, TGF- $\beta$ 3(22/23) $\beta$ 1, TGF- $\beta$ 2(22/23) $\beta$ 3, TGF- $\beta$ 3(22/23) $\beta$ 2 as described hereinafter.

All polymerase chain reactions (PCR) are performed with 50ng of the corresponding TGF- $\beta$ 1, TGF- $\beta$ 2 or

TGF- $\beta$ 3 template. Amplification is performed in the presence of 2 x 2 $\mu$ g of the respective oligomers in a 100 $\mu$ l reaction mixture containing 10mM TRIS/HCl (pH8.35), 50mM KCl, 1.5mM MgCl<sub>2</sub>, 0.05% (w/v) NP40, 0.05% (w/v) Tween 20 and 200 $\mu$ M of each dATP, dGTP, dCTP and dTTP using 5 units Vent Polymerase (New England Biolabs). 30 rounds of amplification are performed under the following temperatures using a Perkin-Elmer Cetus Heating Block: 93 °C/0.1 minutes, 45 °C/0.2 minutes, 73 °C/1.5 minutes.

For the construction of all DNA molecules encoding any of the above-referenced TGF- $\beta$  hybrid molecules, following oligomers are used which are corresponding to modified nucleotide sequences of the cDNAs (see SEQ ID NO. 1, 2 and 3) of

- TGF- $\beta$ 1: oligomers 1 and 2, SEQ ID NO. 10 and 11, respectively,
- TGF- $\beta$ 2: oligomers 3 and 4, SEQ ID NO. 12 and 13, respectively, and
- TGF- $\beta$ 3: oligomers 5 and 6, SEQ ID NO. 14 and 15, respectively.

These oligonucleotides represent the 5' (oligomers 1,3 and 5) and 3' (2,4 and 6) sequences which flank the regions coding for the mature forms (112 amino acids) of the respective protein. In addition, oligomers 7 to 36 (see SEQ ID Nos. 16 to 45) which correspond to nucleotide sequences within highly conserved coding region in the respective TGF- $\beta$ 1, TGF- $\beta$ 2 and TGF- $\beta$ 3 cDNA molecules are also synthesized.

For the construction of the DNA molecules encoding the TGF- $\beta$ 1(44/45) $\beta$ 2, TGF- $\beta$ 2(44/45) $\beta$ 1, TGF- $\beta$ 1(44/45) $\beta$ 3, TGF- $\beta$ 3(44/45) $\beta$ 1, TGF- $\beta$ 2(44/45) $\beta$ 3, and TGF- $\beta$ 3(44/45) $\beta$ 2, all having the hinge points between amino acids 44 and 45, oligomers 7, 8, 11, 12, 9 and 10, corresponding to SEQ ID NO. 16, 17, 20, 21, 18, and 19, respectively, are used in addition to oligomers 1 to 6.

Using oligomers 1 and 8, a 146 bp long fragment which includes the coding region of the first 44 amino acids at the N-terminus of the TGF- $\beta$ 1 mature form protein is amplified in a first PCR reaction from a TGF- $\beta$ 1 cDNA template. The second moiety of the hybrid TGF- $\beta$  cDNA is likewise generated in a second PCR reaction using oligomers 7 and 4, resulting in the amplification of a 241bp long fragment from a TGF- $\beta$ 2 cDNA template which includes the coding region of the last 68 amino acids at the C-terminus of the TGF- $\beta$ 2 mature form protein. The PCR reactions are phenol/chloroform extracted and ethanol precipitated. The amplification products are then dissolved in 10mM TRIS/HCl(pH 7.5), 1 mM EDTA and gel filtrated over a A-15m Biogel column (Bio Rad). In a third PCR reaction, using oligomers 1 and 4, these amplification products are pooled to form the template for the generation of the hybrid TGF- $\beta$ 1(44/45) $\beta$ 2 cDNA.

Likewise, TGF- $\beta$ 1(44/45) $\beta$ 3, TGF- $\beta$ 2(44/45) $\beta$ 1, TGF- $\beta$ 2(44/45) $\beta$ 3, TGF- $\beta$ 3(44/45) $\beta$ 1 and TGF- $\beta$ 3(44/45) $\beta$ 2 hybrids are generated in three PCR reactions according to the method described above but using the oligomers and templates ("templ. cDNA") listed in the table below.

	<u>1st PCR React.</u>		<u>2nd PCR React.</u>		<u>3rd PCR React.</u>	
	Oligo-	templ.	Oligo-	templ.	Oligo-	templ.
TGF- $\beta$ Hybrid	mers	cDNA	mers	cDNA	mers	cDNA
$\beta$ 1 (44/45) $\beta$ 2	1 & 8	TGF- $\beta$ 1	7 & 4	TGF- $\beta$ 2	1 & 4	*
$\beta$ 1 (44/45) $\beta$ 3	1 & 8	TGF- $\beta$ 1	7 & 6	TGF- $\beta$ 3	1 & 6	*
$\beta$ 2 (44/45) $\beta$ 1	3 & 12	TGF- $\beta$ 2	11 & 2	TGF- $\beta$ 1	3 & 2	*
$\beta$ 2 (44/45) $\beta$ 3	3 & 12	TGF- $\beta$ 2	11 & 6	TGF- $\beta$ 3	3 & 6	*
$\beta$ 3 (44/45) $\beta$ 1	5 & 10	TGF- $\beta$ 3	9 & 2	TGF- $\beta$ 1	5 & 2	*
$\beta$ 3 (44/45) $\beta$ 2	5 & 10	TGF- $\beta$ 3	9 & 4	TGF- $\beta$ 2	5 & 4	*

\* in each example, the reaction products from the 1st and 2nd PCR reactions form the DNA template for the 3rd PCR reaction.

For the construction of hybrids TGF- $\beta$ 1(22/23) $\beta$ 2, TGF- $\beta$ 2(22/23) $\beta$ 1, TGF- $\beta$ 1(22/23) $\beta$ 3, TGF- $\beta$ 3(22/23) $\beta$ 1, TGF- $\beta$ 2(22/23) $\beta$ 3, and TGF- $\beta$ 3(22/23) $\beta$ 2, all having the hinge point between amino acid 22 and 23, also oligomers 1 to 6 and additionally the following oligonucleotides are used which correspond to modified nucleotide sequences of

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- TGF- $\beta$ 1: oligo 13 and 14 (SEQ ID NO. 22 and 23, respectively)
- TGF- $\beta$ 2: oligo 15 and 16 (SEQ ID NO. 24 and 25, respectively)
- TGF- $\beta$ 3: oligo 17 and 18 (SEQ ID NO. 26 and 27, respectively).

The hybrids are generated in three PCR reactions according to the method described above but using the oligomers and templates ("templ. cDNA") listed in the table below.

	TGF- $\beta$ Hybrid	<u>1st PCR React.</u>		<u>2nd PCR React.</u>		<u>3rd PCR React.</u>	
		Oligo- mers	templ. cDNA	Oligo- mers	templ. cDNA	Oligo- mers	templ. cDNA
	$\beta$ 1 (22/23) $\beta$ 2	1 & 14	TGF- $\beta$ 1	13 & 4	TGF- $\beta$ 2	1 & 4	*
	$\beta$ 1 (22/23) $\beta$ 3	1 & 14	TGF- $\beta$ 1	13 & 6	TGF- $\beta$ 3	1 & 6	*
	$\beta$ 2 (22/23) $\beta$ 1	3 & 16	TGF- $\beta$ 2	15 & 2	TGF- $\beta$ 1	3 & 2	*
	$\beta$ 2 (22/23) $\beta$ 3	3 & 16	TGF- $\beta$ 2	15 & 6	TGF- $\beta$ 3	3 & 6	*
	$\beta$ 3 (22/23) $\beta$ 1	5 & 18	TGF- $\beta$ 3	17 & 2	TGF- $\beta$ 1	5 & 2	*
	$\beta$ 3 (22/23) $\beta$ 2	5 & 18	TGF- $\beta$ 3	17 & 4	TGF- $\beta$ 2	5 & 4	*

\* in each example, the reaction products from the 1st and 2nd PCR reactions form the DNA template for the 3rd PCR reaction.

For the construction of hybrids TGF- $\beta$ 1(56/57) $\beta$ 2, TGF- $\beta$ 2(56/57) $\beta$ 1, TGF- $\beta$ 1(56/57) $\beta$ 3, TGF- $\beta$ 3(56/57) $\beta$ 1, TGF- $\beta$ 2(56/57) $\beta$ 3, and TGF- $\beta$ 3(56/57) $\beta$ 2, all having the hinge point between amino acid 56 and 57, also oligomers 1 to 6 and additionally the following oligonucleotides are used which correspond to modified nucleotide sequences of

- TGF- $\beta$ 1: oligo 19 and 20 (SEQ ID NO. 28 and 29, respectively)
- TGF- $\beta$ 2: oligo 21 and 22 (SEQ ID NO. 30 and 31, respectively)
- TGF- $\beta$ 3: oligo 23 and 24 (SEQ ID NO. 32 and 33, respectively)

The hybrids are generated in three PCR reactions according to the method described above but using the oligomers and templates ("templ. cDNA") listed in the table below.

	TGF- $\beta$ Hybrid	<u>1st PCR React.</u>		<u>2nd PCR React.</u>		<u>3rd PCR React.</u>	
		Oligo- mers	templ. cDNA	Oligo- mers	templ. cDNA	Oligo- mers	templ. cDNA
	$\beta$ 1 (56/57) $\beta$ 2	1 & 20	TGF- $\beta$ 1	19 & 4	TGF- $\beta$ 2	1 & 4	*
	$\beta$ 1 (56/57) $\beta$ 3	1 & 20	TGF- $\beta$ 1	19 & 6	TGF- $\beta$ 3	1 & 6	*
	$\beta$ 2 (56/57) $\beta$ 1	3 & 22	TGF- $\beta$ 2	21 & 2	TGF- $\beta$ 1	3 & 2	*
	$\beta$ 2 (56/57) $\beta$ 3	3 & 22	TGF- $\beta$ 2	21 & 6	TGF- $\beta$ 3	3 & 6	*
	$\beta$ 3 (56/57) $\beta$ 1	5 & 24	TGF- $\beta$ 3	23 & 2	TGF- $\beta$ 1	5 & 2	*
	$\beta$ 3 (56/57) $\beta$ 2	5 & 24	TGF- $\beta$ 3	23 & 4	TGF- $\beta$ 2	5 & 4	*

\* in each example, the reaction products from the 1st and 2nd PCR reactions form the DNA template for the 3rd PCR reaction.

For the construction of hybrids TGF- $\beta$ 1(79/80) $\beta$ 2, TGF- $\beta$ 2(79/80) $\beta$ 1, TGF- $\beta$ 1(79/80) $\beta$ 3, TGF- $\beta$ 3(79/80) $\beta$ 1, TGF- $\beta$ 2(79/80) $\beta$ 3, and TGF- $\beta$ 3(79/80) $\beta$ 2, all having the hinge point between amino acid 79 and 80, also oligomers 1 to 6 and additionally the following oligonucleotides are used which correspond to modified nucleotide sequences of

- TGF- $\beta$ 1: oligo 25 and 26 (SEQ ID NO. 34 and 35, respectively)
- TGF- $\beta$ 2: oligo 27 and 28 (SEQ ID NO. 36 and 37, respectively)
- TGF- $\beta$ 3: oligo 29 and 30 (SEQ ID NO. 38 and 39, respectively).

The hybrids are generated in three PCR reactions according to the method described above but using the oligomers and templates ("templ. cDNA") listed in the table below.

TGF- $\beta$ Hybrid	1st PCR React.		2nd PCR React.		3rd PCR React.	
	Oligomers	templ. cDNA	Oligomers	templ. cDNA	Oligomers	templ. cDNA
$\beta$ 1 (79/80) $\beta$ 2	1 & 26	TGF- $\beta$ 1	25 & 4	TGF- $\beta$ 2	1 & 4	*
$\beta$ 1 (79/80) $\beta$ 3	1 & 26	TGF- $\beta$ 1	25 & 6	TGF- $\beta$ 3	1 & 6	*
$\beta$ 2 (79/80) $\beta$ 1	3 & 28	TGF- $\beta$ 2	27 & 2	TGF- $\beta$ 1	3 & 2	*
$\beta$ 2 (79/80) $\beta$ 3	3 & 28	TGF- $\beta$ 2	27 & 6	TGF- $\beta$ 3	3 & 6	*
$\beta$ 3 (79/80) $\beta$ 1	5 & 30	TGF- $\beta$ 3	29 & 2	TGF- $\beta$ 1	5 & 2	*
$\beta$ 3 (79/80) $\beta$ 2	5 & 30	TGF- $\beta$ 3	29 & 4	TGF- $\beta$ 2	5 & 4	*

\* in each example, the reaction products from the 1st and 2nd PCR reactions form the DNA template for the 3rd PCR reaction.

For the construction of hybrids TGF- $\beta$ 1(90/91) $\beta$ 2, TGF- $\beta$ 2(90/91) $\beta$ 1, TGF- $\beta$ 1(90/91) $\beta$ 3, TGF- $\beta$ 3(90/91) $\beta$ 1, TGF- $\beta$ 2(90/91) $\beta$ 3, and TGF- $\beta$ 3(90/91) $\beta$ 2, all having the hinge point between amino acid 90 and 91, also oligomers 1 to 6 and additionally the following oligonucleotides are used which correspond to modified nucleotide sequences of

- TGF- $\beta$ 1: oligo 31 and 32 (SEQ ID NO. 40 and 41, respectively)
- TGF- $\beta$ 2: oligo 33 and 34 (SEQ ID NO. 42 and 43, respectively)
- TGF- $\beta$ 3: oligo 35 and 36 (SEQ ID NO. 44 and 45, respectively).

The hybrids are generated in three PCR reactions according to the method described above but using the oligomers and templates ("templ. cDNA") listed in the table below.

		<u>1st PCR React.</u>		<u>2nd PCR React.</u>		<u>3rd PCR React.</u>	
		Oligo-	templ.	Oligo-	templ.	Oligo-	templ.
5	TGF- $\beta$						
	Hybrid	mers	cDNA	mers	cDNA	mers	cDNA
	$\beta 1$ (90/91) $\beta 2$	1 & 32	TGF- $\beta 1$	31 & 4	TGF- $\beta 2$	1 & 4	*
	$\beta 1$ (90/91) $\beta 3$	1 & 32	TGF- $\beta 1$	31 & 6	TGF- $\beta 3$	1 & 6	*
10	$\beta 2$ (90/91) $\beta 1$	3 & 34	TGF- $\beta 2$	33 & 2	TGF- $\beta 1$	3 & 2	*
	$\beta 2$ (90/91) $\beta 3$	3 & 34	TGF- $\beta 2$	33 & 6	TGF- $\beta 3$	3 & 6	*
	$\beta 3$ (90/91) $\beta 1$	5 & 36	TGF- $\beta 3$	35 & 2	TGF- $\beta 1$	5 & 2	*
15	$\beta 3$ (90/91) $\beta 2$	5 & 36	TGF- $\beta 3$	35 & 4	TGF- $\beta 2$	5 & 4	*

\* in each example, the reaction products from the 1st and 2nd PCR reactions form the DNA template for the 3rd PCR reaction.

In each case the third PCR reaction is phenol/chloroform extracted and ethanol precipitated. The precipitate is then digested to completion with NcoI and Sall following the recommendations of the supplier (Boehringer). The hybrid TGF- $\beta$  cDNA molecule is purified by gel electrophoresis (Ultrapure BRL) using NA-45 DEAE paper (Schleicher and Schuell). The DNA is eluted from the paper in 50mM TRIS/HCl (pH7.5), 5mM EDTA, 1M NaCl and is then phenol/chloroform extracted and ethanol precipitated. The resulting hybrid TGF- $\beta$  DNA pellets is washed with 70% ethanol, resuspended in 10mM TRIS/HCl (pH7.5), 1mM EDTA and then sub-cloned into plasmid pGEM-5zf(+) (Promega) via the NcoI and Sall sites.

The constructs resulting from the preparation of the DNA encoding the hybrids with the hinge point between amino acid 44 and 45 are designated as pGKM.D98(TGF- $\beta 1$ (44/45) $\beta 2$ ) pGKM.D571(TGF- $\beta 2$ (44/45) $\beta 1$ ), pGKM.D99(TGF- $\beta 1$ (44/45) $\beta 3$ ), pGKM.D584(TGF- $\beta 3$ (44/45) $\beta 1$ ), pGKM.D580(TGF- $\beta 2$ (44/45) $\beta 3$ ) and pGKM.D619(TGF- $\beta 3$ (44/45) $\beta 2$ ) and are used to transform competent E.coli JM109 cells (see Example 2). Clones carrying the correct inserts encoding the hybrid TGF- $\beta 1$ (44/45) $\beta 2$ , TGF- $\beta 2$ (44/45) $\beta 1$ , TGF- $\beta 1$ (44/45) $\beta 3$ , TGF- $\beta 3$ (44/45) $\beta 1$ , TGF- $\beta 2$ (44/45) $\beta 3$  and TGF- $\beta 3$ (44/45) $\beta 2$  are designated as E.coli JM109 pGKM.D98(TGF- $\beta 1$ (44/45) $\beta 2$ ), E.coli JM109 pGKM.D571(TGF- $\beta 2$ (44/45) $\beta 1$ ), E.coli JM109 pGKM.D99(TGF- $\beta 1$ (44/45) $\beta 3$ ), E.coli JM109 pGKM.D584(TGF- $\beta 3$ (44/45) $\beta 1$ ), E.coli JM109 pGKM.D580(TGF- $\beta 2$ (44/45) $\beta 3$ ) and E.coli JM109 pGKM.D619(TGF- $\beta 3$ (44/45) $\beta 2$ ), respectively.

Likewise the constructs resulting from the preparation of the DNA encoding the hybrids with the hinge point between amino acids 56 and 57 are designated as pGKM.D98(TGF- $\beta 1$ (56/57) $\beta 2$ ) pGKM.D571(TGF- $\beta 2$ (56/57) $\beta 1$ ), pGKM.D99(TGF- $\beta 1$ (56/57) $\beta 3$ ), pGKM.D584(TGF- $\beta 3$ (56/57) $\beta 1$ ), pGKM.D580(TGF- $\beta 2$ (56/57) $\beta 3$ ), and pGKM.D619(TGF- $\beta 3$ (56/57) $\beta 2$ ) and are used to transform competent E.coli JM109 cells (see Example 2). Clones carrying the correct inserts encoding the hybrid TGF- $\beta 1$ (56/57) $\beta 2$ , TGF- $\beta 2$ (56/57) $\beta 1$ , TGF- $\beta 1$ (56/57) $\beta 3$ , TGF- $\beta 3$ (56/57) $\beta 1$ , TGF- $\beta 2$ (56/57) $\beta 3$  and TGF- $\beta 3$ (56/57) $\beta 2$  are designated as E.coli JM109 pGKM.D98(TGF- $\beta 1$ (56/57) $\beta 2$ ), E.coli JM109 pGKM.D571(TGF- $\beta 2$ (56/57) $\beta 1$ ), E.coli JM109 pGKM.D99(TGF- $\beta 1$ (56/57) $\beta 3$ ), E.coli JM109 pGKM.D584(TGF- $\beta 3$ (56/57) $\beta 1$ ), E.coli JM109 pGKM.D580(TGF- $\beta 2$ (56/57) $\beta 3$ ), and E.coli JM109 pGKM.D619(TGF- $\beta 3$ (56/57) $\beta 2$ ), respectively.

Likewise the constructs resulting from the preparation of the DNA encoding the hybrids with the hinge point between amino acids 79 and 80 are designated as pGKM.D98(TGF- $\beta 1$ (79/80) $\beta 2$ ) pGKM.D571(TGF- $\beta 2$ (79/80) $\beta 1$ ), pGKM.D99(TGF- $\beta 1$ (79/80) $\beta 3$ ), pGKM.D584(TGF- $\beta 3$ (79/80) $\beta 1$ ), pGKM.D580(TGF- $\beta 2$ (79/80) $\beta 3$ ), and pGKM.D619(TGF- $\beta 3$ (79/80) $\beta 2$ ) and are used to transform competent E.coli JM109 cells (see Example 2). Clones carrying the correct inserts encoding the hybrid TGF- $\beta 1$ (79/80) $\beta 2$ , TGF- $\beta 2$ (79/80) $\beta 1$ , TGF- $\beta 1$ (79/80) $\beta 3$ , TGF- $\beta 3$ (79/80) $\beta 1$ , TGF- $\beta 2$ (79/80) $\beta 3$  and TGF- $\beta 3$ (79/80) $\beta 2$  are designated as E.coli JM109 pGKM.D98(TGF- $\beta 1$ (79/80) $\beta 2$ ), E.coli JM109 pGKM.D571(TGF- $\beta 2$ (79/80) $\beta 1$ ), E.coli JM109 pGKM.D99(TGF- $\beta 1$ (79/80) $\beta 3$ ), E.coli JM109 pGKM.D584(TGF- $\beta 3$ (79/80) $\beta 1$ ), E.coli JM109 pGKM.D580(TGF- $\beta 2$ (79/80) $\beta 3$ ), and E.coli JM109 pGKM.D619(TGF- $\beta 3$ (79/80) $\beta 2$ ), respectively.

Likewise, the constructs resulting from the preparation of the DNA encoding the hybrids with the hinge point between amino acids 90 and 91 are designated as pGKM.D98(TGF- $\beta 1$ (90/91) $\beta 2$ ) pGKM.D571(TGF- $\beta 2$ (90/91) $\beta 1$ ), pGKM.D99(TGF- $\beta 1$ (90/91) $\beta 3$ ), pGKM.D584(TGF- $\beta 3$ (90/91) $\beta 1$ ), pGKM.D580(TGF- $\beta 2$ (90/91) $\beta 3$ ) and

pGKM.D619(TGF- $\beta$ 3(90/91) $\beta$ 2) and are used to transform competent *E.coli* JM109 cells (see Example 2). Clones carrying the correct inserts encoding the hybrid TGF- $\beta$ 1(90/91) $\beta$ 2, TGF- $\beta$ 2(90/91) $\beta$ 1, TGF- $\beta$ 1(90/91) $\beta$ 3, TGF- $\beta$ 3(90/91) $\beta$ 1, TGF- $\beta$ 2(90/91) $\beta$ 3 and TGF- $\beta$ 3(90/91) $\beta$ 2 are designated as *E.coli* JM109 pGKM.D98(TGF- $\beta$ 1(90/91) $\beta$ 2), *E.coli* JM109 pGKM.D571(TGF- $\beta$ 2(90/91) $\beta$ 1), *E.coli* JM109 pGKM.D99(TGF- $\beta$ 1(90/91) $\beta$ 3), *E.coli* JM109 pGKM.D584(TGF- $\beta$ 3(90/91) $\beta$ 1), *E.coli* JM109 pGKM.D580(TGF- $\beta$ 2(90/91) $\beta$ 3) and *E.coli* JM109 pGKM.D619(TGF- $\beta$ 3(90/91) $\beta$ 2), respectively.

Likewise, the constructs resulting from the preparation of the DNA encoding the hybrids with the hinge point between amino acid 22 and 23 are designated as pGKM.D98(TGF- $\beta$ 1(22/23) $\beta$ 2) pGKM.D571 (TGF- $\beta$ 2(22/23) $\beta$ 1), pGKM.D99(TGF- $\beta$ 1(22/23) $\beta$ 3), pGKM.D584(TGF- $\beta$ 3(22/23) $\beta$ 1), pGKM.D580(TGF- $\beta$ 2(22/23) $\beta$ 3) and pGKM.D619(TGF- $\beta$ 3(22/23) $\beta$ 2) and are used to transform competent *E.coli* JM109 cells (see Example 2). Clones carrying the correct inserts encoding the hybrid TGF- $\beta$ 1(22/23) $\beta$ 2, TGF- $\beta$ 2(22/23) $\beta$ 1, TGF- $\beta$ 1(22/23) $\beta$ 3, TGF- $\beta$ 3(22/23) $\beta$ 1, TGF- $\beta$ 2(22/23) $\beta$ 3 and TGF- $\beta$ 3(22/23) $\beta$ 2 are designated as *E.coli* JM109 pGKM.D98(TGF- $\beta$ 1(22/23) $\beta$ 2), *E.coli* JM109 pGKM.D571(TGF- $\beta$ 2(22/23) $\beta$ 1), *E.coli* JM109 pGKM.D99(TGF- $\beta$ 1(22/23) $\beta$ 3), *E.coli* JM109 pGKM.D584(TGF- $\beta$ 3(22/23) $\beta$ 1), *E.coli* JM109 pGKM.D580(TGF- $\beta$ 2(22/23) $\beta$ 3) and *E.coli* JM109 pGKM.D619(TGF- $\beta$ 3(22/23) $\beta$ 2), respectively.

#### Example 2: Sequencing of hybrid TGF- $\beta$ cDNAs

Identities of the various hybrid TGF- $\beta$  cDNAs are confirmed by double-stranded sequencing according to the Sanger-method [PNAS 74:5463(1977)] using oligomers 7,8,9,10,11, and 12, standard SP6 and T7 primers (Promega) and a Sequenase kit (U.S.Biochemicals). The nucleotide sequence covering the 112 amino acids of the mature TGF- $\beta$ 1(44/45) $\beta$ 2, TGF- $\beta$ 1(44/45) $\beta$ 3, TGF- $\beta$ 2(44/45) $\beta$ 1, TGF- $\beta$ 2(44/45) $\beta$ 3, TGF- $\beta$ 3(44/45) $\beta$ 1 and TGF- $\beta$ 3(44/45) $\beta$ 2 hybrids, plus an additional methionine residue at the N-terminus, are depicted under SEQ ID NO.4,5,6,7,8 and 9, respectively (start codon ATG not shown).

#### Example 3: Expression of hybrid TGF- $\beta$ s in *E.coli*

##### 3A.General Methods

##### Bacterial strain (*E. coli* K12):

LC 137:  $htrR_{am}$ ,  $lonR_{g}$ ,  $lac_{am}$ ,  $mal_{am}$ ,  $trp_{am}$ ,  $pho_{am}$ ,  $rspL$ ,  $tsx::Tn10$ ,  $supC_{ts}$  (Goff, S.A. et al. (1984) PNAS 81, 6647-6651).

##### Plasmids:

pPLMu: (Buell, G. et al. (1985) Nucleic Acids Res. 13, 1923-1938). This plasmid carries the bacteriophage  $\lambda$   $P_L$  promoter with the phage  $\mu_{ner}$  gene ribosome binding site (Van Leerdam, E. et al. (1982) Virology 123, 19-28).

pcl<sub>67</sub>: Plasmid encoding a thermolabile  $\lambda$ CI<sub>67</sub> repressor and conferring resistance to kanamycin (Remault, E. et al. (1983) Gene 22, 103-113).

##### SDS gel-electrophoresis:

SDS polyacrylamide gel-electrophoresis (SDS-PAGE) and protein staining is done as described previously (Laemmli, U.K. (1970) Nature 227, 680-685) using the Miniprotean II cell from BIORAD) and 1 mm thick 18 % polyacrylamide gels.

##### Heat induction:

7 ml of LB-Medium (Maniatis et al. (1982), Molecular Cloning, Cold Spring Harbor Laboratory, New York) in a 20 ml culture tube containing 40  $\mu$ g of each ampicillin and kanamycin (LB/amp/kan) are inoculated with a single colony and incubated with shaking overnight at 30°C. 5 ml of this overnight culture are added to 15 ml of LB/amp/kan in a 100 ml Erlenmeyer flask. This flask is transferred to a 42°C waterbath shaker. A 2 ml sample is taken before transfer (non-inducing conditions) and 1 ml samples at 1 hour intervals after the transfer (inducing conditions). Cells are pelleted by centrifugation (5 min, 10.000 rpm in an Eppendorf centrifuge) and the supernatant is discarded. The pellet is resuspended in 100  $\mu$ l of sample buffer for SDS-PAGE and heated for 10 min at 95°C. 5  $\mu$ l aliquots are loaded for SDS-PAGE.

Preparation of competent cells:

Competent *E. coli* cells are prepared by the conventional calcium chloride procedure as described in Maniatis et al. (1982), Molecular Cloning, Cold Spring Harbor Laboratory, New York. Cells carrying plasmid pCL857 are grown at 30°C.

3B. Construction of expression vectors and expression of hybrid TGF- $\beta$ s

*E. coli* JM109 is transformed with the pGEM-5zf(+) vectors which contain the corresponding TGF- $\beta$ 1(44/45) $\beta$ 2, TGF- $\beta$ 2(44/45) $\beta$ 1, TGF- $\beta$ 1(44/45) $\beta$ 3, TGF- $\beta$ 3(44/45) $\beta$ 1, TGF- $\beta$ 2(44/45) $\beta$ 3 and TGF- $\beta$ 3(44/45) $\beta$ 2 hybrid DNAs. The *E. coli* cells are grown in LB medium and plasmid DNA is prepared. In each case 5  $\mu$ g of plasmid hybrid TGF- $\beta$  DNA are cut to completion in 50  $\mu$ l restriction buffer with NcoI and Sall following the recommendations of the supplier (Boehringer). The DNA is precipitated by addition of 5  $\mu$ l 3M sodium acetate, 100mM MgCl<sub>2</sub>, 5mM EDTA, and 150  $\mu$ l Ethanol. After incubation at -70 °C for 15min the DNA is pelleted by centrifugation at 13.000g for 15 min in a SS-34 rotor in a Sorvall centrifuge. The supernatant is discarded and the pellet is resuspended in 80  $\mu$ l 0.089 M TRIS-Borate, 0.089 M Boric Acid and 0.002 M EDTA (TBE Buffer) containing 0.25% Bromphenol Blue and 0.25% Xylene Cyanol. 4 x 20  $\mu$ l samples are electrophoresed through a 1 % Agarose gel in TBE Buffer containing 0.5  $\mu$ g/ml Ethidium Bromide at 50 volts until the Bromphenol Blue marker reaches the bottom of the 10 cm long and 0.8 cm-thick gel. The DNA fragments coding for the mature TGF- $\beta$ 1(44/45) $\beta$ 2, TGF- $\beta$ 2(44/45) $\beta$ 1, TGF- $\beta$ 1(44/45) $\beta$ 3, TGF- $\beta$ 3(44/45) $\beta$ 1, TGF- $\beta$ 2(44/45) $\beta$ 3 and TGF- $\beta$ 3(44/45) $\beta$ 2 hybrids respectively, are visualised under short wave U.V. light, cut out with a razor blade and electroeluted from a gel piece in a Schleicher and Schuell Biotrap Apparatus applying 200 milliamps for 1.5 h. The eluted DNA fragments are precipitated (see above) and resuspended in 20  $\mu$ l TE.

5  $\mu$ l of plasmid pPLMu are linearized by digestion with NcoI and Sall and gel purified as described above for the fragment DNAs. 100ng of the linearized and purified pPLMu vector DNA and 3x the molar equivalent of the respective purified fragment DNA are incubated at 4 °C for 15 h in 20  $\mu$ l ligation buffer (70 mM TRIS-HCl, pH7.5, 10mM MgCl<sub>2</sub>, 5mM DTT, 0.1mM Adenosine-triphosphate) containing 1 unit of DNA ligase (Boehringer).

10  $\mu$ l of the ligation mixture are added to 200  $\mu$ l of cold (4 °C) competent *E. coli* LC137 cells carrying plasmid pCL857. After 30 min the cells are heat shocked by incubation for 1.5 min in a 42 °C water bath. 2ml of LB medium are added and the culture is shaken for 60 min at 30 °C. 200  $\mu$ l aliquots are plated on LB plates containing Ampicillin and Kanamycin and incubated for 22 h at 30 °C. Single colonies are cultivated and plasmid DNA is analysed. Subcloning of the DNA fragments coding for TGF- $\beta$ 1(44/45) $\beta$ 2, TGF- $\beta$ 2(44/45) $\beta$ 1, TGF- $\beta$ 1(44/45) $\beta$ 3, TGF- $\beta$ 3(44/45) $\beta$ 1, TGF- $\beta$ 2(44/45) $\beta$ 3 and TGF- $\beta$ 3(44/45) $\beta$ 2 in pPLMu results in plasmids pPLMu.TGF- $\beta$ 1(44/45) $\beta$ 2, pPLMu.TGF- $\beta$ 2(44/45) $\beta$ 1, pPLMu.TGF- $\beta$ 1(44/45) $\beta$ 3, pPLMu.TGF- $\beta$ 3(44/45) $\beta$ 1, pPLMu.TGF- $\beta$ 2(44/45) $\beta$ 3 and pPLMu.TGF- $\beta$ 3(44/45) $\beta$ 2, respectively. Clones containing the above constructs are referred to as *E. coli*LC137/pPLMu.TGF- $\beta$ 1(44/45) $\beta$ 2, *E. coli*LC137/pPLMu.TGF- $\beta$ 2(44/45) $\beta$ 1, *E. coli*LC137/pPLMu.TGF- $\beta$ 1(44/45) $\beta$ 3, *E. coli*LC137/pPLMu.TGF- $\beta$ 3(44/45) $\beta$ 1, *E. coli*LC137/pPLMu.TGF- $\beta$ 2(44/45) $\beta$ 3 and *E. coli*LC137/pPLMu.TGF- $\beta$ 3(44/45) $\beta$ 2, respectively.

Likewise, DNA fragments coding for TGF- $\beta$ 1(56/57) $\beta$ 2, TGF- $\beta$ 2(56/57) $\beta$ 1, TGF- $\beta$ 1(56/57) $\beta$ 3, TGF- $\beta$ 3(56/57) $\beta$ 1, TGF- $\beta$ 2(56/57) $\beta$ 3 and TGF- $\beta$ 3(56/57) $\beta$ 2 are subcloned in pPLMu to construct plasmids pPLMu.TGF- $\beta$ 1(56/57) $\beta$ 2, pPLMu.TGF- $\beta$ 2(56/57) $\beta$ 1, pPLMu.TGF- $\beta$ 1(56/57) $\beta$ 3, pPLMu.TGF- $\beta$ 3(56/57) $\beta$ 1, pPLMu.TGF- $\beta$ 2(56/57) $\beta$ 3 and pPLMu.TGF- $\beta$ 3(56/57) $\beta$ 2 and transformed hosts *E. coli*LC137/pPLMu.TGF- $\beta$ 1(56/57) $\beta$ 2, *E. coli*LC137/pPLMu.TGF- $\beta$ 2(56/57) $\beta$ 1, *E. coli*LC137/pPLMu.TGF- $\beta$ 1(56/57) $\beta$ 3, *E. coli*LC137/pPLMu.TGF- $\beta$ 3(56/57) $\beta$ 1, *E. coli*LC137/pPLMu.TGF- $\beta$ 2(56/57) $\beta$ 3 and *E. coli*LC137/pPLMu.TGF- $\beta$ 3(56/57) $\beta$ 2 are prepared.

Likewise, DNA fragments coding for TGF- $\beta$ 1(79/80) $\beta$ 2, TGF- $\beta$ 2(79/80) $\beta$ 1, TGF- $\beta$ 1(79/80) $\beta$ 3, TGF- $\beta$ 3(79/80) $\beta$ 1, TGF- $\beta$ 2(79/80) $\beta$ 3 and TGF- $\beta$ 3(79/80) $\beta$ 2 are subcloned in pPLMu to construct plasmids pPLMu.TGF- $\beta$ 1(79/80) $\beta$ 2, pPLMu.TGF- $\beta$ 2(79/80) $\beta$ 1, pPLMu.TGF- $\beta$ 1(79/80) $\beta$ 3, pPLMu.TGF- $\beta$ 3(79/80) $\beta$ 1, pPLMu.TGF- $\beta$ 2(79/80) $\beta$ 3 and pPLMu.TGF- $\beta$ 3(79/80) $\beta$ 2 and transformed hosts *E. coli*LC137/pPLMu.TGF- $\beta$ 1(79/80) $\beta$ 2, *E. coli*LC137/pPLMu.TGF- $\beta$ 2(79/80) $\beta$ 1, *E. coli*LC137/pPLMu.TGF- $\beta$ 1(79/80) $\beta$ 3, *E. coli*LC137/pPLMu.TGF- $\beta$ 3(79/80) $\beta$ 1, *E. coli*LC137/pPLMu.TGF- $\beta$ 2(79/80) $\beta$ 3 and *E. coli*LC137/pPLMu.TGF- $\beta$ 3(79/80) $\beta$ 2 are prepared.

Likewise, DNA fragments coding for TGF- $\beta$ 1(90/91) $\beta$ 2, TGF- $\beta$ 2(90/91) $\beta$ 1, TGF- $\beta$ 1(90/91) $\beta$ 3, TGF- $\beta$ 3(90/91) $\beta$ 1, TGF- $\beta$ 2(90/91) $\beta$ 3 and TGF- $\beta$ 3(90/91) $\beta$ 2 are subcloned in pPLMu to construct plasmids pPLMu.TGF- $\beta$ 1(90/91) $\beta$ 2, pPLMu.TGF- $\beta$ 2(90/91) $\beta$ 1, pPLMu.TGF- $\beta$ 1(90/91) $\beta$ 3, pPLMu.TGF- $\beta$ 3(90/91) $\beta$ 1, pPLMu.TGF- $\beta$ 2(90/91) $\beta$ 3 and pPLMu.TGF- $\beta$ 3(90/91) $\beta$ 2 and transformed hosts *E. coli*LC137/pPLMu.TGF- $\beta$ 1(90/91) $\beta$ 2, *E. coli*LC137/pPLMu.TGF- $\beta$ 2(90/91) $\beta$ 1, *E. coli*LC137/pPLMu.TGF- $\beta$ 1(90/91) $\beta$ 3, *E. coli*LC137/pPLMu.TGF- $\beta$ 3(90/91) $\beta$ 1, *E. coli*LC137/pPLMu.TGF- $\beta$ 2(90/91) $\beta$ 3 and *E. coli*LC137/pPLMu.TGF- $\beta$ 3(90/91) $\beta$ 2 are prepared.

pPLMu.TGF- $\beta$ 3(90/91) $\beta$ 1, E.coliLC137/pPLMu.TGF- $\beta$ 2(90/91) $\beta$ 3 and E.coliLC137/pPLMu.TGF- $\beta$ 3(90/91) $\beta$ 2 are prepared.

Likewise, DNA fragments coding for TGF- $\beta$ 1(22/23) $\beta$ 2, TGF- $\beta$ 2(22/23) $\beta$ 1, TGF- $\beta$ 1(22/23) $\beta$ 3, TGF- $\beta$ 3(22/23) $\beta$ 1, TGF- $\beta$ 2(22/23) $\beta$ 3 and TGF- $\beta$ 3(22/23) $\beta$ 2 are subcloned in pPLMu to construct plasmids pPLMu.TGF- $\beta$ 1(22/23) $\beta$ 2, pPLMu.TGF- $\beta$ 2(22/23) $\beta$ 1, pPLMu.TGF- $\beta$ 1(22/23) $\beta$ 3, pPLMu.TGF- $\beta$ 3(22/23) $\beta$ 1, pPLMu.TGF- $\beta$ 2(22/23) $\beta$ 3 and pPLMu.TGF- $\beta$ 3(22/23) $\beta$ 2 and transformed hosts E.coliLC137/pPLMu.TGF- $\beta$ 1(22/23) $\beta$ 2, E.coliLC137/pPLMu.TGF- $\beta$ 2(22/23) $\beta$ 1, E.coliLC137/pPLMu.TGF- $\beta$ 1(22/23) $\beta$ 3, E.coliLC137/pPLMu.TGF- $\beta$ 3(22/23) $\beta$ 1, E.coliLC137/pPLMu.TGF- $\beta$ 2(22/23) $\beta$ 3 and E.coliLC137/pPLMu.TGF- $\beta$ 3(22/23) $\beta$ 2 are prepared.

E.coliLC137/pPLMu.TGF- $\beta$ 1(44/45) $\beta$ 2, E.coliLC137/pPLMu.TGF- $\beta$ 2(44/45) $\beta$ 1, E.coliLC137/pPLMu.TGF- $\beta$ 1(44/45) $\beta$ 3, E.coliLC137/pPLMu.TGF- $\beta$ 3(44/45) $\beta$ 1, E.coliLC137/pPLMu.TGF- $\beta$ 2(44/45) $\beta$ 3 and E.coliLC137/pPLMu.TGF- $\beta$ 3(44/45) $\beta$ 2 are heat induced (see example 3.A) and the expressed proteins are analysed by SDS-PAGE. TGF- $\beta$ 1(44/45) $\beta$ 2, TGF- $\beta$ 2(44/45) $\beta$ 1, TGF- $\beta$ 1(44/45) $\beta$ 3, TGF- $\beta$ 3(44/45) $\beta$ 1, TGF- $\beta$ 2(44/45) $\beta$ 3 and TGF- $\beta$ 3(44/45) $\beta$ 2 all appear as heat induced proteins 2 h after heat induction migrating with an apparent molecular weight of approximately 12.000 D.

Likewise, E.coliLC137/pPLMu.TGF- $\beta$ 1(56/57) $\beta$ 2, E.coliLC137/pPLMu.TGF- $\beta$ 2(56/57) $\beta$ 1, E.coliLC137/pPLMu.TGF- $\beta$ 1(56/57) $\beta$ 3, E.coliLC137/pPLMu.TGF- $\beta$ 3(56/57) $\beta$ 1, E.coliLC137/pPLMu.TGF- $\beta$ 2(56/57) $\beta$ 3 and E.coliLC137/pPLMu.TGF- $\beta$ 3(56/57) $\beta$ 2 are heat induced (see example 3.A) and the expressed proteins are analysed by SDS-PAGE. TGF- $\beta$ 1(56/57) $\beta$ 2, TGF- $\beta$ 2(56/57) $\beta$ 1, TGF- $\beta$ 1(56/57) $\beta$ 3, TGF- $\beta$ 3(56/57) $\beta$ 1, TGF- $\beta$ 2(56/57) $\beta$ 3 and TGF- $\beta$ 3(56/57) $\beta$ 2 all appear as heat induced proteins 2 h after heat induction migrating with an apparent molecular weight of approximately 12.000 D.

Likewise, E.coliLC137/pPLMu.TGF- $\beta$ 1(79/80) $\beta$ 2, E.coliLC137/pPLMu.TGF- $\beta$ 2(79/80) $\beta$ 1, E.coliLC137/pPLMu.TGF- $\beta$ 1(79/80) $\beta$ 3, E.coliLC137/pPLMu.TGF- $\beta$ 3(79/80) $\beta$ 1, E.coliLC137/pPLMu.TGF- $\beta$ 2(79/80) $\beta$ 3 and E.coliLC137/pPLMu.TGF- $\beta$ 3(79/80) $\beta$ 2 are heat induced (see example 3.A) and the expressed proteins are analysed by SDS-PAGE. TGF- $\beta$ 1(79/80) $\beta$ 2, TGF- $\beta$ 2(79/80) $\beta$ 1, TGF- $\beta$ 1(79/80) $\beta$ 3, TGF- $\beta$ 3(79/80) $\beta$ 1, TGF- $\beta$ 2(79/80) $\beta$ 3 and TGF- $\beta$ 3(79/80) $\beta$ 2 all appear as heat induced proteins 2 h after heat induction migrating with an apparent molecular weight of approximately 12.000 D.

Likewise, E.coliLC137/pPLMu.TGF- $\beta$ 1(90/91) $\beta$ 2, E.coliLC137/pPLMu.TGF- $\beta$ 2(90/91) $\beta$ 1, E.coliLC137/pPLMu.TGF- $\beta$ 1(90/91) $\beta$ 3, E.coliLC137/pPLMu.TGF- $\beta$ 3(90/91) $\beta$ 1, E.coliLC137/pPLMu.TGF- $\beta$ 2(90/91) $\beta$ 3 and E.coliLC137/pPLMu.TGF- $\beta$ 3(90/91) $\beta$ 2 are heat induced (see example 3.A) and the expressed proteins are analysed by SDS-PAGE. TGF- $\beta$ 1(90/91) $\beta$ 2, TGF- $\beta$ 2(90/91) $\beta$ 1, TGF- $\beta$ 1(90/91) $\beta$ 3, TGF- $\beta$ 3(90/91) $\beta$ 1, TGF- $\beta$ 2(90/91) $\beta$ 3 and TGF- $\beta$ 3(90/91) $\beta$ 2 all appear as heat induced proteins 2 h after heat induction migrating with an apparent molecular weight of approximately 12.000 D.

Likewise, E.coliLC137/pPLMu.TGF- $\beta$ 1(22/23) $\beta$ 2, E.coliLC137/pPLMu.TGF- $\beta$ 2(22/23) $\beta$ 1, E.coliLC137/pPLMu.TGF- $\beta$ 1(22/23) $\beta$ 3, E.coliLC137/pPLMu.TGF- $\beta$ 3(22/23) $\beta$ 1, E.coliLC137/pPLMu.TGF- $\beta$ 2(22/23) $\beta$ 3 and E.coliLC137/pPLMu.TGF- $\beta$ 3(22/23) $\beta$ 2 are heat induced (see example 3.A) and the expressed proteins are analysed by SDS-PAGE. TGF- $\beta$ 1(22/23) $\beta$ 2, TGF- $\beta$ 2(22/23) $\beta$ 1, TGF- $\beta$ 1(22/23) $\beta$ 3, TGF- $\beta$ 3(22/23) $\beta$ 1, TGF- $\beta$ 2(22/23) $\beta$ 3 and TGF- $\beta$ 3(22/23) $\beta$ 2 all appear as heat induced proteins 2 h after heat induction migrating with an apparent molecular weight of approximately 12.000 D.

### 3C.Fermentation of Transformants

Overnight cultures of E.coliLC137/pPLMu.TGF- $\beta$ 1(44/45) $\beta$ 2, E.coliLC137/pPLMu.TGF- $\beta$ 2(44/45) $\beta$ 1, E.coliLC137/pPLMu.TGF- $\beta$ 1(44/45) $\beta$ 3, E.coliLC137/pPLMu.TGF- $\beta$ 3(44/45) $\beta$ 1, E.coliLC137/pPLMu.TGF- $\beta$ 2(44/45) $\beta$ 3 and E.coliLC137/pPLMu.TGF- $\beta$ 3(44/45) $\beta$ 2 in 2 l Erlenmeyer flasks containing 750 ml of LB medium with 40 mg/l of Ampicillin and Kanamycin are grown at 30 °C. 300 ml of the overnight cultures are added to 750 ml of LB medium containing antibiotics as mentioned above in 2 l Erlenmeyer flasks and heated to 42 °C by shaking for approximately 3.5 min in a 65 °C water bath. The flasks are then transferred to a 42 °C shaker and incubated for 3 h. The flasks are cooled down to 12 °C in an ice water bath and the cells are collected after centrifugation for 10 min at 8.000 rpm in a GSA rotor (Sorvall).

Likewise, hybrid proteins are produced by means of E.coliLC137/pPLMu.TGF- $\beta$ 1(56/57) $\beta$ 2, E.coliLC137/pPLMu.TGF- $\beta$ 2(56/57) $\beta$ 1, E.coliLC137/pPLMu.TGF- $\beta$ 1(56/57) $\beta$ 3, E.coliLC137/pPLMu.TGF- $\beta$ 3(56/57) $\beta$ 1, E.coliLC137/pPLMu.TGF- $\beta$ 2(56/57) $\beta$ 3, and E.coliLC137/pPLMu.TGF- $\beta$ 3(56/57) $\beta$ 2.

Likewise, hybrid proteins are produced by means of E.coliLC137/pPLMu.TGF- $\beta$ 1(79/80) $\beta$ 2, E.coliLC137/pPLMu.TGF- $\beta$ 2(79/80) $\beta$ 1, E.coliLC137/pPLMu.TGF- $\beta$ 1(79/80) $\beta$ 3, E.coliLC137/pPLMu.TGF- $\beta$ 3(79/80) $\beta$ 1, E.coliLC137/pPLMu.TGF- $\beta$ 2(79/80) $\beta$ 3, and E.coliLC137/pPLMu.TGF- $\beta$ 3(79/80) $\beta$ 2.

Likewise, hybrid proteins are produced by means of E.coliLC137/pPLMu.TGF- $\beta$ 1(90/91) $\beta$ 2, E.coliLC137/pPLMu.TGF- $\beta$ 2(90/91) $\beta$ 1, E.coliLC137/pPLMu.TGF- $\beta$ 1(90/91) $\beta$ 3, E.coliLC137/pPLMu.TGF- $\beta$ 3(90/91) $\beta$ 1, E.coliLC137/pPLMu.TGF- $\beta$ 2(90/91) $\beta$ 3, and E.coliLC137/pPLMu.TGF- $\beta$ 3(90/91) $\beta$ 2.

E.coliLC137/pPLMu.TGF- $\beta$ 2(90/91) $\beta$ 3, and E.coliLC137/pPLMu.TGF- $\beta$ 3(90/91) $\beta$ 2.

Likewise, hybrid proteins are produced by means of E.coliLC137/pPLMu.TGF- $\beta$ 1(22/23) $\beta$ 2, E.coliLC137/pPLMu.TGF- $\beta$ 2(22/23) $\beta$ 1, E.coliLC137/pPLMu.TGF- $\beta$ 1(22/23) $\beta$ 3, E.coliLC137/pPLMu.TGF- $\beta$ 3(22/23) $\beta$ 1, E.coliLC137/pPLMu.TGF- $\beta$ 2(22/23) $\beta$ 3, and E.coliLC137/pPLMu.TGF- $\beta$ 3(22/23) $\beta$ 2

**Example 4: Expression of TGF- $\beta$ 1/ $\beta$ 2 TGF- $\beta$ 2/ $\beta$ 1, TGF- $\beta$ 1/ $\beta$ 3, TGF- $\beta$ 3/ $\beta$ 1, TGF- $\beta$ 2/ $\beta$ 3 and TGF- $\beta$ 3/ $\beta$ 2 in *Saccharomyces cerevisiae***

The coding sequences of mature TGF- $\beta$ 1(44/45) $\beta$ 2, TGF- $\beta$ 2(44/45) $\beta$ 1, TGF- $\beta$ 1(44/45) $\beta$ 3, TGF- $\beta$ 3(44/45) $\beta$ 1, TGF- $\beta$ 2(44/45) $\beta$ 3 and TGF- $\beta$ 3(44/45) $\beta$ 2 are expressed in *Saccharomyces cerevisiae* under the control of the inducible promoter of the yeast acid phosphatase (PH05). They are obtained from plasmids pPLMu.TGF- $\beta$ 1(44/45) $\beta$ 2, pPLMu.TGF- $\beta$ 2(44/45) $\beta$ 1, pPLMu.TGF- $\beta$ 1(44/45) $\beta$ 3, pPLMu.TGF- $\beta$ 3(44/45) $\beta$ 1, pPLMu.TGF- $\beta$ 2(44/45) $\beta$ 3 and pPLMu.TGF- $\beta$ 3(44/45) $\beta$ 2, respectively.

The expression vectors are constructed in two steps:

A. construction of plasmid pJDB207/PH05-RIT-12,

B. construction of plasmids pJDB207R/PH05-TGF- $\beta$ 1(44/45) $\beta$ 2, pJDB207R/PH05-TGF- $\beta$ 2(44/45) $\beta$ 1, pJDB207R/PH05-TGF- $\beta$ 1(44/45) $\beta$ 3, pJDB207R/PH05-TGF- $\beta$ 3(44/45) $\beta$ 1, pJDB207R/PH05-TGF- $\beta$ 2(44/45) $\beta$ 3 and pJDB207R/PH05-TGF- $\beta$ 3(44/45) $\beta$ 2, where A) provides the yeast vector and the PH05 transcriptional terminator and B) provides the expression cassettes with an insert coding for mature TGF- $\beta$ 1(44/45) $\beta$ 2, TGF- $\beta$ 2(44/45) $\beta$ 1, TGF- $\beta$ 1(44/45) $\beta$ 3, TGF- $\beta$ 3(44/45) $\beta$ 1, TGF- $\beta$ 2(44/45) $\beta$ 3 and TGF- $\beta$ 3(44/45) $\beta$ 2, respectively, under the control of the PH05 promoter.

**A. Construction of plasmid pJDB207/PH05-RIT-12**

Plasmid p31R/SS-TPA $\Delta$ 2 (DSM 4295) is digested with restriction endonucleases EcoRI and XhoI. The 4.2 kb vector fragment is isolated by preparative agarose gel electrophoresis.

The four oligodeoxyribonucleotides I-1 (see SEQ ID No. 46), I-2 (SEQ ID No. 47), I-3 (SEQ ID No. 48) and I-4 (SEQ ID No. 49) are synthesized by a DNA synthesizer (model 380B Applied Biosystem) and purified on a 12% polyacrylamide gel containing 8 M urea. A solution of 10 pmoles of each of the four oligodeoxyribonucleotides I-1, I-2, I-3 and I-4 in 10  $\mu$ l of 0.5 M Tris-HCl pH8 is incubated at 95 °C for 5 min on a water bath. The water bath is slowly cooled to 30 °C over a period of 5 h in order to anneal the complementary oligonucleotides. To this annealed mixture is added 2  $\mu$ l each of 0.1 M MgCl<sub>2</sub>, 0.1 M NaCl, 30 mM DTT, 4 mM ATP and 8 U of polynucleotide kinase (Boehringer). Kinase is carried out at 37 °C for 1 h.

The annealed, kinased oligonucleotides and 60 pmoles of the 4.2 kb EcoRI-XhoI vector fragment of p31R/SS-TPA $\Delta$ 2 are ligated with T4 DNA ligase. The ligation mixture is used to transform competent *E. coli* HB101 cells.

Amp<sup>R</sup> colonies are picked, plasmid DNA is prepared, digested with EcoRI and XhoI, radiolabelled at the EcoRI end and analysed on a 6% polyacrylamide gel containing 8M urea using HaeIII cut radiolabelled pBR322 as marker. One of the clones with correct band size is grown in LB, the plasmid is isolated and referred to as p31 RIT-12.

Plasmid p31 RIT-12 is linearized with restriction endonuclease Sall. Partial HindIII digestion in the presence of ethidiumbromide results in a 1 kb Sall/HindIII fragment comprising the 276 bp Sall/BamHI pBR322 sequence, the 534 bp promoter of the yeast acid phosphatase PH05, the yeast invertase signal sequence (coding for 19 amino acids) and the PH05 transcriptional terminator.

The 1 kb Sall/HindIII fragment of p31RIT-12 is cloned in to the yeast-*E.coli* shuttle vector pJDB207 (DSM 6782), which had been cut with Sall and HindIII. The resulting plasmid containing the 1 kb insert is referred to as pJDB207/PH05-RIT-12.

**B. Construction of plasmid pJDB207R/PH05-TGF- $\beta$ 1(44/45) $\beta$ 2**

Plasmid pPLMu.TGF- $\beta$ 1(44/45) $\beta$ 2 is cut with NcoI. The sticky ends are filled in a reaction with Klenow DNA polymerase. EcoRI linker (5'-CCGGAATTCGG; Biolabs) are added and the mixture is ligated. The resulting circular plasmid is referred to as pGKMA668 (TGF- $\beta$ 1(44/45) $\beta$ 2) and is cut with EcoRI and Sall. A 0.4 kb EcoRI/Sall fragment is isolated from an agarose gel, purified and resuspended in sterile water at a concentration of 25  $\mu$ g/ml. The fragment contains the mature coding sequence of TGF- $\beta$ 1(44/45) $\beta$ 2 with an ATG in frame to codon GCT which defines amino acid Ala 1 of mature TGF- $\beta$ 1(44/45) $\beta$ 2.

The PH05 promoter is isolated from plasmid p31RIT 12 (see above) on a 534 bp BamHI/EcoRI fragment. Plasmid pJDB207/PH05-RIT-12 is cut with BamHI and XhoI. The large, 6.8 kb BamHI/XhoI fragment is isolated.

The PH05 transcriptional terminator remains on the fragment. The BamHI/EcoRI PH05 promoter fragment, the EcoRI/Sall fragment coding for TGF- $\beta$ 2, and the BamHI/XhoI vector fragment are ligated. One correct clone with the TGF- $\beta$ 2 gene under the control of the PH05 promoter cloned in an anticlockwise orientation into pJDB207 is referred to as pJDB207R/PH05-TGF- $\beta$ 1(44/45) $\beta$ 2.

5 In an analogous manner, mature TGF- $\beta$ 2(44/45) $\beta$ 1, TGF- $\beta$ 1(44/45) $\beta$ 3, TGF- $\beta$ 3(44/45) $\beta$ 1, TGF- $\beta$ 2(44/45) $\beta$ 3 and TGF- $\beta$ 3(44/45) $\beta$ 2 are expressed in *S. cerevisiae*. Plasmids containing the coding sequences of TGF- $\beta$ 1 and TGF- $\beta$ 3 are specified hereinbefore. After digestion of these plasmids with NcoI, addition of EcoRI linkers and ligation, the resulting circular plasmids are cut with EcoRI and Sall. The EcoRI/Sall fragments are cloned into pJDB207 as described above. The resulting plasmids are referred to as pJDB207R/PH05-TGF- $\beta$ 2(44/45) $\beta$ 1, pJDB207R/PH05-TGF- $\beta$ 1(44/45) $\beta$ 3, pJDB207R/PH05-TGF- $\beta$ 3(44/45) $\beta$ 1, pJDB207R/PH05-TGF- $\beta$ 2(44/45) $\beta$ 3 and pJDB207R/PH05-TGF- $\beta$ 3(44/45) $\beta$ 2.

In an analogous manner the expression vectors pJDB207R/PH05-TGF- $\beta$ 1(56/57) $\beta$ 2, pJDB207R/PH05-TGF- $\beta$ 2(56/57) $\beta$ 1, pJDB207R/PH05-TGF- $\beta$ 1(56/57) $\beta$ 3, pJDB207R/PH05-TGF- $\beta$ 3(56/57) $\beta$ 1, pJDB207R/PH05-TGF- $\beta$ 2(56/57) $\beta$ 3, and pJDB207R/PH05-TGF- $\beta$ 3(56/57) $\beta$ 2 are produced from pPLMu.TGF- $\beta$ 1(56/57) $\beta$ 2, pPLMu.TGF- $\beta$ 2(56/57) $\beta$ 1, pPLMu.TGF- $\beta$ 1(56/57) $\beta$ 3, pPLMu.TGF- $\beta$ 3(56/57) $\beta$ 1, pPLMu.TGF- $\beta$ 2(56/57) $\beta$ 3, and pPLMu.TGF- $\beta$ 3(56/57) $\beta$ 2 respectively, in order to express the coding sequences of mature TGF- $\beta$ 1(56/57) $\beta$ 2, TGF- $\beta$ 2(56/57) $\beta$ 1, TGF- $\beta$ 1(56/57) $\beta$ 3, TGF- $\beta$ 3(56/57) $\beta$ 1, TGF- $\beta$ 2(56/57) $\beta$ 3 and TGF- $\beta$ 3(56/57) $\beta$ 2.

15 In an analogous manner the expression vectors pJDB207R/PH05-TGF- $\beta$ 1(79/80) $\beta$ 2, pJDB207R/PH05-TGF- $\beta$ 2(79/80) $\beta$ 1, pJDB207R/PH05-TGF- $\beta$ 1(79/80) $\beta$ 3, pJDB207R/PH05-TGF- $\beta$ 3(79/80) $\beta$ 1, pJDB207R/PH05-TGF- $\beta$ 2(79/80) $\beta$ 3 and pJDB207R/PH05-TGF- $\beta$ 3(79/80) $\beta$ 2 are produced from pPLMu.TGF- $\beta$ 1(79/80) $\beta$ 2, pPLMu.TGF- $\beta$ 2(79/80) $\beta$ 1, pPLMu.TGF- $\beta$ 1(79/80) $\beta$ 3, pPLMu.TGF- $\beta$ 3(79/80) $\beta$ 1, pPLMu.TGF- $\beta$ 2(79/80) $\beta$ 3 and pPLMu.TGF- $\beta$ 3(79/80) $\beta$ 2, respectively, in order to express the coding sequences of mature TGF- $\beta$ 1(79/80) $\beta$ 2, TGF- $\beta$ 2(79/80) $\beta$ 1, TGF- $\beta$ 1(79/80) $\beta$ 3, TGF- $\beta$ 3(79/80) $\beta$ 1, TGF- $\beta$ 2(79/80) $\beta$ 3 and TGF- $\beta$ 3(79/80) $\beta$ 2.

In an analogous manner the expression vectors pJDB207R/PH05-TGF- $\beta$ 1(90/91) $\beta$ 2, pJDB207R/PH05-TGF- $\beta$ 2(90/91) $\beta$ 1, pJDB207R/PH05-TGF- $\beta$ 1(90/91) $\beta$ 3, pJDB207R/PH05-TGF- $\beta$ 3(90/91) $\beta$ 1, pJDB207R/PH05-TGF- $\beta$ 2(90/91) $\beta$ 3 and pJDB207R/PH05-TGF- $\beta$ 3(90/91) $\beta$ 2 are produced from pPLMu.TGF- $\beta$ 1(90/91) $\beta$ 2, pPLMu.TGF- $\beta$ 2(90/91) $\beta$ 1, pPLMu.TGF- $\beta$ 1(90/91) $\beta$ 3, pPLMu.TGF- $\beta$ 3(90/91) $\beta$ 1, pPLMu.TGF- $\beta$ 2(90/91) $\beta$ 3 and pPLMu.TGF- $\beta$ 3(90/91) $\beta$ 2, respectively, in order to express the coding sequences of mature TGF- $\beta$ 1(90/91) $\beta$ 2, TGF- $\beta$ 2(90/91) $\beta$ 1, TGF- $\beta$ 1(90/91) $\beta$ 3, TGF- $\beta$ 3(90/91) $\beta$ 1, TGF- $\beta$ 2(90/91) $\beta$ 3 and TGF- $\beta$ 3(90/91) $\beta$ 2.

30 In an analogous manner the expression vectors pJDB207R/PH05-TGF- $\beta$ 1(22/23) $\beta$ 2, pJDB207R/PH05-TGF- $\beta$ 2(22/23) $\beta$ 1, pJDB207R/PH05-TGF- $\beta$ 1(22/23) $\beta$ 3, pJDB207R/PH05-TGF- $\beta$ 3(22/23) $\beta$ 1, pJDB207R/PH05-TGF- $\beta$ 2(22/23) $\beta$ 3 and pJDB207R/PH05-TGF- $\beta$ 3(22/23) $\beta$ 2 are produced from pPLMu.TGF- $\beta$ 1(22/23) $\beta$ 2, pPLMu.TGF- $\beta$ 2(22/23) $\beta$ 1, pPLMu.TGF- $\beta$ 1(22/23) $\beta$ 3, pPLMu.TGF- $\beta$ 3(22/23) $\beta$ 1, pPLMu.TGF- $\beta$ 2(22/23) $\beta$ 3 and pPLMu.TGF- $\beta$ 3(22/23) $\beta$ 2, respectively, in order to express the coding sequences of mature TGF- $\beta$ 1(22/23) $\beta$ 2, TGF- $\beta$ 2(22/23) $\beta$ 1, TGF- $\beta$ 1(22/23) $\beta$ 3, TGF- $\beta$ 3(22/23) $\beta$ 1, TGF- $\beta$ 2(22/23) $\beta$ 3 and TGF- $\beta$ 3(22/23) $\beta$ 2.

#### C. Transformation of *S. cerevisiae* strain GRF18

*Saccharomyces cerevisiae* strain GRF18 (MAT $\alpha$ , his3-11, his3-15, leu2-3, leu2-112, can<sup>R</sup>, DSM 3665) is transformed with plasmids pJDB207R/PH05-TGF- $\beta$ 1(44/45) $\beta$ 2, pJDB207R/PH05-TGF- $\beta$ 2(44/45) $\beta$ 1, pJDB207R/PH05-TGF- $\beta$ 1(44/45) $\beta$ 3, pJDB207R/PH05-TGF- $\beta$ 3(44/45) $\beta$ 1, pJDB207R/PH05-TGF- $\beta$ 2(44/45) $\beta$ 3 or pJDB207R/PH05-TGF- $\beta$ 3(44/45) $\beta$ 2, using the transformation protocol described by Hinnen, A. et al. (1978) PNAS 75, 1929. Transformed yeast cells are selected on yeast minimal medium plates deficient in leucine. Single transformed yeast colonies are isolated and referred to as

45 *Saccharomyces cerevisiae* GRF18/pJDB207R/PH05-TGF- $\beta$ 1(44/45) $\beta$ 2,  
*Saccharomyces cerevisiae* GRF18/pJDB207R/PH05-TGF- $\beta$ 2(44/45) $\beta$ 1,  
*Saccharomyces cerevisiae* GRF18/pJDB207R/PH05-TGF- $\beta$ 1(44/45) $\beta$ 3,  
*Saccharomyces cerevisiae* GRF18/pJDB207R/PH05-TGF- $\beta$ 3(44/45) $\beta$ 1,  
*Saccharomyces cerevisiae* GRF18/pJDB207R/PH05-TGF- $\beta$ 2(44/45) $\beta$ 3, and  
 50 *Saccharomyces cerevisiae* GRF18/pJDB207R/PH05-TGF- $\beta$ 3(44/45) $\beta$ 2.

In an analogous manner *Saccharomyces cerevisiae* strain GRF18 (MAT $\alpha$ , his3-11, his3-15, leu2-3, leu2-112, can<sup>R</sup>, DSM 3665) is transformed with plasmids pJDB207R/PH05-TGF- $\beta$ 1(56/57) $\beta$ 2, pJDB207R/PH05-TGF- $\beta$ 2(56/57) $\beta$ 1, pJDB207R/PH05-TGF- $\beta$ 1(56/57) $\beta$ 3, pJDB207R/PH05-TGF- $\beta$ 3(56/57) $\beta$ 1, pJDB207R/PH05-TGF- $\beta$ 2(56/57) $\beta$ 3 and pJDB207R/PH05-TGF- $\beta$ 3(56/57) $\beta$ 2. Transformed yeast cells are selected on yeast minimal medium plates deficient in leucine. Single transformed yeast colonies are isolated and referred to as  
 55 *Saccharomyces cerevisiae* GRF18/pJDB207R/PH05-TGF- $\beta$ 1(56/57) $\beta$ 2,  
*Saccharomyces cerevisiae* GRF18/pJDB207R/PH05-TGF- $\beta$ 2(56/57) $\beta$ 1,  
*Saccharomyces cerevisiae* GRF18/pJDB207R/PH05-TGF- $\beta$ 1(56/57) $\beta$ 3,

Saccharomyces cerevisiae GRF18/pJDB207R/PH05-TGF- $\beta$ 3(56/57) $\beta$ 1,  
Saccharomyces cerevisiae GRF18/pJDB207R/PH05-TGF- $\beta$ 2(56/57) $\beta$ 3, and  
Saccharomyces cerevisiae GRF18/pJDB207R/PH05-TGF- $\beta$ 3(56/57) $\beta$ 2.

In an analogous manner Saccharomyces cerevisiae strain GRF18 (MAT $\alpha$ , his3-11, his3-15, leu2-3, leu2-112, can<sup>R</sup>, DSM 3665) is transformed with plasmids pJDB207R/PH05-TGF- $\beta$ 1(79/80) $\beta$ 2, pJDB207R/PH05-TGF- $\beta$ 2(79/80) $\beta$ 1, pJDB207R/PH05-TGF- $\beta$ 1(79/80) $\beta$ 3, pJDB207R/PH05-TGF- $\beta$ 3(79/80) $\beta$ 1, pJDB207R/PH05-TGF- $\beta$ 2(79/80) $\beta$ 3 and pJDB207R/PH05-TGF- $\beta$ 3(79/80) $\beta$ 2. Transformed yeast cells are selected on yeast minimal medium plates deficient in leucine. Single transformed yeast colonies are isolated and referred to as

Saccharomyces cerevisiae GRF18/pJDB207R/PH05-TGF- $\beta$ 1(79/80) $\beta$ 2,  
Saccharomyces cerevisiae GRF18/pJDB207R/PH05-TGF- $\beta$ 2(79/80) $\beta$ 1,  
Saccharomyces cerevisiae GRF18/pJDB207R/PH05-TGF- $\beta$ 1(79/80) $\beta$ 3,  
Saccharomyces cerevisiae GRF18/pJDB207R/PH05-TGF- $\beta$ 3(79/80) $\beta$ 1,  
Saccharomyces cerevisiae GRF18/pJDB207R/PH05-TGF- $\beta$ 2(79/80) $\beta$ 3, and  
Saccharomyces cerevisiae GRF18/pJDB207R/PH05-TGF- $\beta$ 3(79/80) $\beta$ 2.

In an analogous manner Saccharomyces cerevisiae strain GRF18 (MAT $\alpha$ , his3-11, his3-15, leu2-3, leu2-112, can<sup>R</sup>, DSM 3665) is transformed with plasmids pJDB207R/PH05-TGF- $\beta$ 1(90/91) $\beta$ 2, pJDB207R/PH05-TGF- $\beta$ 2(90/91) $\beta$ 1, pJDB207R/PH05-TGF- $\beta$ 1(90/91) $\beta$ 3, pJDB207R/PH05-TGF- $\beta$ 3(90/91) $\beta$ 1, pJDB207R/PH05-TGF- $\beta$ 2(90/91) $\beta$ 3 and pJDB207R/PH05-TGF- $\beta$ 3(90/91) $\beta$ 2. Transformed yeast cells are selected on yeast minimal medium plates deficient in leucine. Single transformed yeast colonies are isolated and referred to as

Saccharomyces cerevisiae GRF18/pJDB207R/PH05-TGF- $\beta$ 1(90/91) $\beta$ 2,  
Saccharomyces cerevisiae GRF18/pJDB207R/PH05-TGF- $\beta$ 2(90/91) $\beta$ 1,  
Saccharomyces cerevisiae GRF18/pJDB207R/PH05-TGF- $\beta$ 1(90/91) $\beta$ 3,  
Saccharomyces cerevisiae GRF18/pJDB207R/PH05-TGF- $\beta$ 3(90/91) $\beta$ 1,  
Saccharomyces cerevisiae GRF18/pJDB207R/PH05-TGF- $\beta$ 2(90/91) $\beta$ 3 and  
Saccharomyces cerevisiae GRF18/pJDB207R/PH05-TGF- $\beta$ 3(90/91) $\beta$ 2.

In an analogous manner Saccharomyces cerevisiae strain GRF18 (MAT $\alpha$ , his3-11, his3-15, leu2-3, leu2-112, can<sup>R</sup>, DSM 3665) is transformed with plasmids pJDB207R/PH05-TGF- $\beta$ 1(22/23) $\beta$ 2, pJDB207R/PH05-TGF- $\beta$ 2(22/23) $\beta$ 1, pJDB207R/PH05-TGF- $\beta$ 1(22/23) $\beta$ 3, pJDB207R/PH05-TGF- $\beta$ 3(22/23) $\beta$ 1, pJDB207R/PH05-TGF- $\beta$ 2(22/23) $\beta$ 3 and pJDB207R/PH05-TGF- $\beta$ 3(22/23) $\beta$ 2. Transformed yeast cells are selected on yeast minimal medium plates deficient in leucine. Single transformed yeast colonies are isolated and referred to as

Saccharomyces cerevisiae GRF18/pJDB207R/PH05-TGF- $\beta$ 1(22/23) $\beta$ 2,  
Saccharomyces cerevisiae GRF18/pJDB207R/PH05-TGF- $\beta$ 2(22/23) $\beta$ 1,  
Saccharomyces cerevisiae GRF18/pJDB207R/PH05-TGF- $\beta$ 1(22/23) $\beta$ 3,  
Saccharomyces cerevisiae GRF18/pJDB207R/PH05-TGF- $\beta$ 3(22/23) $\beta$ 1,  
Saccharomyces cerevisiae GRF18/pJDB207R/PH05-TGF- $\beta$ 2(22/23) $\beta$ 3 and  
Saccharomyces cerevisiae GRF18/pJDB207R/PH05-TGF- $\beta$ 3(22/23) $\beta$ 2.

#### 40 D. Fermentation of *S. cerevisiae* transformants and preparation of cell extracts

The yeast transformants, as mentioned above, contain plasmids with PH05 promoter-controlled expression cassettes and therefore require derepression of the promoter for the expression of the TGF- $\beta$  hybrid molecules. Transformants are each grown in two successive precultures (10 ml and 50 ml) in yeast high P<sub>i</sub> minimal medium prepared according to the recipe of the Difco Yeast Nitrogen Base without amino acids but containing 10 g/l L-asparagine instead of (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub>, 1 g/l L-histidine and 20 g/l glucose. The cells of the second preculture are washed in 0.9 % NaCl and all the cells are used to inoculate 100 ml of low P<sub>i</sub> minimal medium prepared according to the recipe of the Difco Yeast Nitrogen Base medium (without amino acids), but containing 0.03 g/l KH<sub>2</sub>PO<sub>4</sub>, 10 g/l L-asparagine, 1 g/l L-histidine and 20 g/l glucose. The cultures are agitated at 30°C at 180 rpm.

Cells from 10 ml of culture are collected at 5 h, 24 h and 48 h by centrifugation at 3000 rpm and washed once in 0.9 % NaCl. The cell pellet is resuspended in lysis buffer [66 mM potassium phosphate pH 7.4, 4 mM Zwittergent (Calbiochem)], 8 g of glass beads (0.5-0.75 mm in diameter) are added and the suspension is shaken vigorously 4-5 times for 2 min each on a Vortex Mixer in the cold. The cell extract is decanted to get rid of the glass beads. Cell debris in the extract are sedimented by centrifugation for 5 min at 3000 rpm at 4°C. The supernatant and pellets are separated and stored at -20°C.

Example 5: Production of dimeric, biologically active hybrid TGF- $\beta$  proteins

The procedures given below\* for the production of dimeric, biologically active TGF- $\beta$ 1(44/45) $\beta$ 2 hybrid may be applied in analogy for the recovery of other dimeric, biologically active TGF- $\beta$  hybrid proteins.

5 E.coli LC137/pPLMu.TGF- $\beta$ 1(44/45) $\beta$ 2 cells are fermented as described above and inclusion bodies are prepared as follows. Cell disruption and recovery of the inclusion bodies is performed at 4°C. About 18 g of wet cells are suspended in 60 ml of 0.1 M TRIS/HCl, 10 mM EDTA, 1 mM PMSF (Phenyl Methan Sulphonyl Fluoride), pH 8.3 (disruption buffer). The cells are passed two times through a Frenchpress (SLM Instruments, Inc.) according to the manufacturers instructions and the volume is brought to 200 ml with the disruption buffer.  
10 The suspension is centrifuged for 20 min at 15.000 g. The pellet obtained is suspended in 100 ml disruption buffer containing 1 M NaCl and centrifuged for 10 min as above. The pellet is suspended in 100 ml disruption buffer containing 1 % Triton X-100 (Pierce) and again centrifuged for 10 min as above.

0.3 g of the washed pellet is then suspended in 10 ml of 20 mM Tris/HCl, 1 mM EDTA, 1 mM PMSF, 0.1 % DTT, pH 8.0, and stirred with a magnetic stirrer for 1 h at room temperature. The sample is then brought to pH 2.5 with concentrated acetic acid and homogenised in a Teflon tissue homogenizer and centrifuged in a  
15 Centricon H-401 centrifuge (Kontron Instruments) with a fixed angle rotor A.8.24 for 60 min, at 15 °C and 12 000 rpm. The acetic acid of the clear supernatant is exchanged with 10 mM HCl in an Amicon 8010 stirred cell with YM05 filter by repeated concentration and dilution of the solution with 10 mM HCl.  
Individual aliquots of the thus solubilized monomeric TGF- $\beta$ 1(44/45) $\beta$ 2 hybrid in 10 mM HCl are dried in vacuo  
20 and analyzed by SDS polyacrylamide gel electrophoresis under reducing conditions on 15 % polyacrylamide slab gels stained with Coomassie Blue R-250. A band of about 12 000 is obtained.

Another aliquot of the solubilized TGF- $\beta$ 1(44/45) $\beta$ 2 hybrid is evaporated in vacuo, dissolved in 25  $\mu$ l acetic acid and subjected to amino acid sequence determination in a gas phase sequencer model 470A (Applied Biosystems). The N-terminal amino acid sequence thus obtained corresponds with the N-terminus of TGF- $\beta$ 1 (see  
25 SEQ ID NO. 1).

6 ml of the solution of TGF- $\beta$ 1(44/45) $\beta$ 2 obtained above, i.e. 1.5 mg of the TGF- $\beta$ 1(44/45) $\beta$ 2, is mixed with 0.14 g CHAPS (Sigma C3023 Lot 80H5018) and precooled at 4 °C. The solution is then slowly added to 7.5 ml of Buffer I (precooled to 4 °C) consisting of 2 M NaCl, 0.2 M Tris, 30 mM CHAPS, 4 mM EDTA, 5 mM Glutathione reduced, pH 8.5. The mixture is stirred for 1 h at room temperature. Then 1.5 ml Buffer II consisting  
30 of 0.1 M Tris, 10 mM Glutathione oxidized, pH 8.0, precooled at 4 °C, is added slowly. The mixture is kept at 4 °C to allow the hybrid TGF- $\beta$ 1(44/45) $\beta$ 2 to refold into the biologically active dimeric form.

After 260 h the refolding process is stopped by adding 4 N HCl to pH 2.5. The sample is dialyzed on an Amicon 8010 stirred cell with YM05 membrane against 10 mM HCl and concentrated to 5 ml and then centrifuged in a MSE table top centrifuge (model centaur 2) for 5 min at 3500 rpm. The clear solution is applied at a  
35 flow rate of 1 ml/min onto a Mono S HR 5/5 column equilibrated in buffer A (20 mM sodium acetate, 30 % isopropanol, pH 4.0) connected to a FPLC chromatography system (Pharmacia) with LCC 500 unit and a UV-MII Detector (Pharmacia) at a wavelength of 280 nm. A linear gradient over 30 min starting at injection time at equilibration conditions and ending with a mixture of 50 % buffer A (20 mM sodium acetate, 30 % Isopropanol, pH 4.0) and 50 % buffer B (corresponds to buffer A with 1 M NaCl).

40 Dimeric active TGF- $\beta$ 1(44/45) $\beta$ 2 is eluted about 8 min. after start of the gradient, collected and concentrated to 1 ml with a Millipore Ultrafree MC unit (5000 NMWL) in a Heraeus Christ Biofuge A at 10 000 rpm. TGF- $\beta$ 1(44/45) $\beta$ 2 is further purified by RP-HPLC using a system consisting of a Vydac C4 214TP5415 column (0.46 cm x 15 cm), two pumps (Waters 510) controlled by Data and Chromatography Control Station (Waters 840) and a UV Detector (Applied Biosystems, model 783) set at 216 nm. The column is equilibrated in 80 %  
45 solvent A (0.1 % TFA in water), 20 % solvent B (0.08 % TFA in acetonitrile). At injection time a linear gradient from 20 to 40 % solvent B in 40 min is applied. The peak with a retention time of 30.25 min is collected and analysed for biological activity as described hereinafter.

Example 6: In vitro activity tests for dimeric, biologically active hybrid TGF- $\beta$  proteins

50 A. BALB/c-3T3 cell migration assay: Purified TGF- $\beta$  hybrids are tested in this previously described assay (Bürk, R.R. (1973) Proc.Natl.Acad.Sci.USA 70:369-372) which measures the number of BALB/c 3T3 cells that have migrated from the monolayer in wounded cultures maintained in serum-free medium for 22 h in the presence or absence of a hybrid TGF- $\beta$ .

55 B. Stimulation of AKR-2B cell DNA synthesis assay: Purified TGF- $\beta$  hybrids are tested in this previously described assay (Graycar, J.L. et al., (1989) Molecular Endocrinology 3:1977-1986) which measures the increase in the levels of [3H]-Thymidine incorporation, over the last 16h of a 66h culture period, in cultures of AKR-2B cells maintained in McCoy's 5A medium containing 5% fetal bovine serum in the presence of

a hybrid TGF- $\beta$ .

C. Inhibition of CCL-64 cell DNA synthesis assay: Purified TGF- $\beta$  hybrids are tested in a modified version of this previously described assay (Graycar, J.L. et al., (1989) Molecular Endocrinology 3:1977-1986) which measures the decrease in the levels of [3H]-Thymidine incorporation, over the last 16h of a 66h culture period, in cultures of CCL-64 cells maintained in DMEM medium containing 5% fetal bovine serum in the presence of a hybrid TGF- $\beta$ .

#### Deposited Microorganisms:

#### Deposition of microorganisms

The following microorganisms were deposited at the Deutsche Sammlung von Mikroorganismen (DSM), Mascheroder Weg 1b, D-3300 Braunschweig (FRG):

microorganism	deposition date	accession number
<u>E. coli</u> LC 137/pPLMu.hTGF- $\beta$ 1	November 28, 1989	DSM 5656
<u>E. coli</u> LC 137/pPLMu.hTGF- $\beta$ 2	November 28, 1989	DSM 5657
<u>E. coli</u> LC 137/pPLMu.hTGF- $\beta$ 3	November 28, 1989	DSM 5658
<u>Saccharomyces cerevisiae</u> GRF 18	March 4, 1986	DSM 3665
<u>E. coli</u> HB101/p31R/SS-TPA $\Delta$ 2	October 23, 1987	DSM 4295
<u>E. coli</u> HB101/pJDB207	November 7, 1991	DSM 6782

Sequence listing

SEQ ID NO. 1

5 Sequence Type: Nucleotide with corresponding polypeptide  
 Sequence Length: 339 base pairs  
 Strandedness: double  
 10 Topology: linear  
 Source: human cDNA  
 Immediate experimental source: E. coli LC 137/pPLMu.hTGF- $\beta$ 1 (DSM 5656)  
 Features: from 1 to 336 coding region for TGF- $\beta$ 1  
 15

20	GCC CTG GAC ACC AAC TAT TGC TTC AGC TCC ACG GAG AAG Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys	39
	5 10	
25	AAC TGC TGC GTG CGG CAG CTG TAC ATT GAC TTC CGC AAG Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys	78
	15 20 25	
30	GAC CTC GGC TGG AAG TGG ATC CAC GAG CCC AAG GGC TAC Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr	117
	30 35	
35	CAT GCC AAC TTC TGC CTC GGG CCC TGC CCC TAC ATT TGG His Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp	156
	40 45 50	
40	AGC CTG GAC ACG CAG TAC AGC AAG GTC CTG GCC CTG TAC Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr	195
	55 60 65	
45	AAC CAG CAT AAC CCG GGC GCC TCG GCG GCG CCG TGC TGC Asn Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys	234
50	70 75	
55		

EP 0 542 679 A1

5 GTG CCG CAG GCG CTG GAG CCG CTG CCC ATC GTG TAC TAC 273  
Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr  
80 85 90

10 GTG GGC CGC AAG CCC AAG GTG GAG CAG CTG TCC AAC ATG 312  
Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met  
95 100

15 ATC GTG CGC TCC TGC AAG TGC AGC TGA 339  
Ile Val Arg Ser Cys Lys Cys Ser  
105 110

20

25 SEQ ID NO. 2  
Sequence Type: Nucleotide with corresponding polypeptide  
Sequence Length: 339 base pairs  
Strandedness: double  
Topology: linear  
30 Source: human cDNA  
Immediate experimental source: E. coli LC 137/pPLMu.hTGF-β2 (DSM 5657)  
Features: from 1 to 336 coding region for TGF-β2

35

GCT TTG GAT GCG GCC TAT TGC TTT AGA AAT GTG CAG GAT 39  
Ala Leu Asp Ala Ala Tyr Cys Phe Arg Asn Val Gln Asp  
40 5 10

AAT TGC TGC CTA CGT CCA CTT TAC ATT GAT TTC AAG AGG 78  
Asn Cys Cys Leu Arg Pro Leu Tyr Ile Asp Phe Lys Arg  
45 15 20 25

GAT CTA GGG TGG AAA TGG ATA CAC GAA CCC AAA GGG TAC 117  
50 Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr  
30 35

55

EP 0 542 679 A1

5 AAT GCC AAC TTC TGT GCT GGA GCA TGC CCG TAT TTA TGG 156  
 Asn Ala Asn Phe Cys Ala Gly Ala Cys Pro Tyr Leu Trp  
 40 45 50  
 10 AGT TCA GAC ACT CAG CAC AGC AGG GTC CTG AGC TTA TAT 195  
 Ser Ser Asp Thr Gln His Ser Arg Val Leu Ser Leu Tyr  
 55 60 65  
 15 AAT ACC ATA AAT CCA GAA GCA TCT GCT TCT CCT TGC TGC 234  
 Asn Thr Ile Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys  
 70 75  
 20 GTG TCC CAA GAT TTA GAA CCT CTA ACC ATT CTC TAC TAC 273  
 Val Ser Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr  
 80 85 90  
 25 ATT GGC AAA ACA CCC AAG ATT GAA CAG CTT TCT AAT ATG 312  
 Ile Gly Lys Thr Pro Lys Ile Glu Gln Leu Ser Asn Met  
 95 100  
 30 ATT GTA AAG TCT TGC AAA TGC AGC TAA 339  
 Ile Val Lys Ser Cys Lys Cys Ser  
 35 105 110

40 SEQ ID NO. 3

Sequence Type: Nucleotide with corresponding polypeptide

Sequence Length: 339 base pairs

Strandedness: double

45 Topology: linear

Source: human cDNA

Immediate experimental source: E. coli LC 137/pPLMu.hTGF-β3 (DSM 5658)

50 Features: from 1 to 336 coding region for TGF-β3

55

EP 0 542 679 A1

5	GCT TTG GAC ACC AAT TAC TGC TTC CGC AAC TTG GAG GAG Ala Leu Asp Thr Asn Tyr Cys Phe Arg Asn Leu Glu Glu	39
	5 10	
10	AAC TGC TGT GTG CGC CCC CTC TAC ATT GAC TTC CGA CAG Asn Cys Cys Val Arg Pro Leu Tyr Ile Asp Phe Arg Gln	78
	15 20 25	
15	GAT CTG GGC TGG AAG TGG GTC CAT GAA CCT AAG GGC TAC Asp Leu Gly Trp Lys Trp Val His Glu Pro Lys Gly Tyr	117
	30 35	
20	TAT GCC AAC TTC TGC TCA GGC CCT TGC CCA TAC CTC CGC Tyr Ala Asn Phe Cys Ser Gly Pro Cys Pro Tyr Leu Arg	156
	40 45 50	
25	AGT GCA GAC ACA ACC CAC AGC ACG GTG CTG GGA CTG TAC Ser Ala Asp Thr Thr His Ser Thr Val Leu Gly Leu Tyr	195
	55 60 65	
30	AAC ACT CTG AAC CCT GAA GCA TCT GCC TCG CCT TGC TGC Asn Thr Leu Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys	234
	70 75	
35	GTG CCC CAG GAC CTG GAG CCC CTG ACC ATC CTG TAC TAT Val Pro Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr	273
40	80 85 90	
45	GTT GGG AGG ACC CCC AAA GTG GAG CAG CTC TCC AAC ATG Val Gly Arg Thr Pro Lys Val Glu Gln Leu Ser Asn Met	312
	95 100	
50	GTG GTG AAG TCT TGT AAA TGT AGC TGA Val Val Lys Ser Cys Lys Cys Ser	339
	105 110	

55

## SEQ ID NO.4

Sequence Type: Nucleotide with corresponding polypeptide

Sequence length: 336 base pairs

Strandedness: double

Topology: linear

Source: human cDNA

Immediate experimental source: E.coli LC 137/pPLMu.TGF-B1(44/45) $\beta$ 2Features: from 1 to 336 coding region for TGF-B1(44/45) $\beta$ 2 hybrid

```

5      GCC CTG GAC ACC AAC TAT TGC TTC AGC TCC ACG GAG AAG      39
      Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys
10      5                                10

15      AAC TGC TGC GTG CGG CAG CTG TAC ATT GAC TTC CGC AAG      78
      Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys
20      15                                20                                25

25      GAC CTC GGC TGG AAG TGG ATC CAC GAG CCC AAG GGC TAC      117
      Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr
30      30                                35

35      CAT GCC AAC TTC TGT GCT GGA GCA TGC CCG TAT TTA TGG      156
      His Ala Asn Phe Cys Ala Gly Ala Cys Pro Tyr Leu Trp
40      40                                45                                50

45      AGT TCA GAC ACT CAG CAC AGC AGG GTC CTG AGC TTA TAT      195
      Ser Ser Asp Thr Gln His Ser Arg Val Leu Ser Leu Tyr
50      55                                60                                65

55      AAT ACC ATA AAT CCA GAA GCA TCT GCT TCT CCT TGC TGC      234
      Asn Thr Ile Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys
70      70                                75

```

5 GTG TCC CAA GAT TTA GAA CCT CTA ACC ATT CTC TAC TAC 273  
 Val Ser Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr  
 80 85 90  
 10 ATT GGC AAA ACA CCC AAG ATT GAA CAG CTT TCT AAT ATG 312  
 Ile Gly Lys Thr Pro Lys Ile Glu Gln Leu Ser Asn Met  
 95 100  
 15 ATT GTA AAG TCT TGC AAA TGC AGC 336  
 Ile Val Lys Ser Cys Lys Cys Ser  
 105 110

SEQ ID NO.5

Sequence Type: Nucleotide with corresponding polypeptide

Sequence length: 336 base pairs

Strandedness: double

Topology: linear

Source: human cDNA

Immediate experimental source: E.coli LC 137/pPLMu.TGF-β1(44/45)β3

Features: from 1 to 336 coding region for TGF-β1(44/45)β3 hybrid

35 GCC CTG GAC ACC AAC TAT TGC TTC AGC TCC ACG GAG AAG 39  
 Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys  
 40 5 10  
 AAC TGC TGC GTG CGG CAG CTG TAC ATT GAC TTC CGC AAG 78  
 Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys  
 45 15 20 25  
 GAC CTC GGC TGG AAG TGG ATC CAC GAG CCC AAG GGC TAC 117  
 50 Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr  
 30 35

EP 0 542 679 A1

5	CAT GCC AAC TTC TGC TCA GGC CCT TGC CCA TAC CTC CGC	156
	His Ala Asn Phe Cys Ser Gly Pro Cys Pro Tyr Leu Arg	
	40 45 50	
10	AGT GCA GAC ACA ACC CAC AGC ACG GTG CTG GGA CTG TAC	195
	Ser Ala Asp Thr Thr His Ser Thr Val Leu Gly Leu Tyr	
	55 60 65	
15	AAC ACT CTG AAC CCT GAA GCA TCT GCC TCG CCT TGC TGC	234
	Asn Thr Leu Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys	
	70 75	
20	GTG CCC CAG GAC CTG GAG CCC CTG ACC ATC CTG TAC TAT	273
	Val Pro Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr	
	80 85 90	
25	GTT GGG AGG ACC CCC AAA GTG GAG CAG CTC TCC AAC ATG	312
	Val Gly Arg Thr Pro Lys Val Glu Gln Leu Ser Asn Met	
	95 100	
30	GTG GTG AAG TCT TGT AAA TGT AGC	336
	Val Val Lys Ser Cys Lys Cys Ser	
	105 110	

SEQ ID NO.6

Sequence Type: Nucleotide with corresponding polypeptide

Sequence length: 336 base pairs

Strandedness: double

Topology: linear

Source: human cDNA

Immediate experimental source: E.coli LC 137/pPLMu.TGF-β2(44/45)β1

Features: from 1 to 336 coding region for TGF-β2(44/45)β1 hybrid

EP 0 542 679 A1

	GCT TTG GAT GCG GCC TAT TGC TTT AGA AAT GTG CAG GAT	39
	Ala Leu Asp Ala Ala Tyr Cys Phe Arg Asn Val Gln Asp	
5	5 10	
	AAT TGC TGC CTA CGT CCA CTT TAC ATT GAT TTC AAG AGG	78
	Asn Cys Cys Leu Arg Pro Leu Tyr Ile Asp Phe Lys Arg	
10	15 20 25	
	GAT CTA GGG TGG AAA TGG ATA CAC GAA CCC AAA GGG TAC	117
	Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr	
15	30 35	
	AAT GCC AAC TTC TGC CTC GGG CCC TGC CCC TAC ATT TGG	156
	Asn Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp	
20	40 45 50	
	AGC CTG GAC ACG CAG TAC AGC AAG GTC CTG GCC CTG TAC	195
	Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr	
25	55 60 65	
	AAC CAG CAT AAC CCG GGC GCC TCG GCG GCG CCG TGC TGC	234
	Asn Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys	
30	70 75	
	GTG CCG CAG GCG CTG GAG CCG CTG CCC ATC GTG TAC TAC	273
	Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr	
35	80 85 90	
	GTG GGC CGC AAG CCC AAG GTG GAG CAG CTG TCC AAC ATG	312
	Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met	
40	95 100	
	ATC GTG CGC TCC TGC AAG TGC AGC	336
	Ile Val Arg Ser Cys Lys Cys Ser	
45	105 110	
50		
55		

## SEQ ID NO.7

Sequence Type: Nucleotide with corresponding polypeptide

Sequence length: 336 base pairs

Strandedness: double

Topology: linear

Source: human cDNA

Immediate experimental source: E.coli LC 137/pPLMu.TGF-β2(44/45)β3

Features: from 1 to 336 coding region for TGF-β2(44/45)β3 hybrid

5 GCT TTG GAT GCG GCC TAT TGC TTT AGA AAT GTG CAG GAT 39  
 Ala Leu Asp Ala Ala Tyr Cys Phe Arg Asn Val Gln Asp  
 10 5 10

20 AAT TGC TGC CTA CGT CCA CTT TAC ATT GAT TTC AAG AGG 78  
 Asn Cys Cys Leu Arg Pro Leu Tyr Ile Asp Phe Lys Arg  
 25 15 20 25

30 GAT CTA GGG TGG AAA TGG ATA CAC GAA CCC AAA GGG TAC 117  
 Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr  
 30 35

35 AAT GCC AAC TTC TGC TCA GGC CCT TGC CCA TAC CTC CGC 156  
 Asn Ala Asn Phe Cys Ser Gly Pro Cys Pro Tyr Leu Arg  
 40 45 50

40 AGT GCA GAC ACA ACC CAC AGC ACG GTG CTG GGA CTG TAC 195  
 Ser Ala Asp Thr Thr His Ser Thr Val Leu Gly Leu Tyr  
 55 60 65

45 AAC ACT CTG AAC CCT GAA GCA TCT GCC TCG CCT TGC TGC 234  
 Asn Thr Leu Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys  
 70 75

55

GTG CCC CAG GAC CTG GAG CCC CTG ACC ATC CTG TAC TAT 273  
 5 Val Pro Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr  
     80                    85                    90

GTT GGG AGG ACC CCC AAA GTG GAG CAG CTC TCC AAC ATG 312  
 10 Val Gly Arg Thr Pro Lys Val Glu Gln Leu Ser Asn Met  
           95                    100

GTG GTG AAG TCT TGT AAA TGT AGC 336  
 15 Val Val Lys Ser Cys Lys Cys Ser  
     105                    110

20

## SEQ ID NO.8

25 Sequence Type: Nucleotide with corresponding polypeptide

Sequence length: 336 base pairs

Strandedness: double

Topology: linear

30

Source: human cDNA

Immediate experimental source: E.coli LC 137/pPLMu.TGF-β3(44/45)β1

Features: from 1 to 336 coding region for TGF-β3(44/45)β1 hybrid

35

GCT TTG GAC ACC AAT TAC TGC TTC CGC AAC TTG GAG GAG 39  
 40 Ala Leu Asp Thr Asn Tyr Cys Phe Arg Asn Leu Glu Glu  
           5                    10

AAC TGC TGT GTG CGC CCC CTC TAC ATT GAC TTC CGA CAG 78  
 45 Asn Cys Cys Val Arg Pro Leu Tyr Ile Asp Phe Arg Gln  
     15                    20                    25

GAT CTG GGC TGG AAG TGG GTC CAT GAA CCT AAG GGC TAC 117  
 50 Asp Leu Gly Trp Lys Trp Val His Glu Pro Lys Gly Tyr  
           30                    35

55

5 TAT GCC AAC TTC TGC CTC GGG CCC TGC CCC TAC ATT TGG 156  
 Tyr Ala Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp  
 40 45 50  
 10 AGC CTG GAC ACG CAG TAC AGC AAG GTC CTG GCC CTG TAC 195  
 Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu Tyr  
 55 60 65  
 15 AAC CAG CAT AAC CCG GGC GCC TCG GCG GCG CCG TGC TGC 234  
 Asn Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys  
 70 75  
 20 GTG CCG CAG GCG CTG GAG CCG CTG CCC ATC GTG TAC TAC 273  
 Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr  
 80 85 90  
 25 GTG GGC CGC AAG CCC AAG GTG GAG CAG CTG TCC AAC ATG 312  
 Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met  
 95 100  
 30 ATC GTG CGC TCC TGC AAG TGC AGC 336  
 Ile Val Arg Ser Cys Lys Cys Ser  
 35 105 110

40 SEQ ID NO.9

Sequence Type: Nucleotide with corresponding polypeptide

Sequence length: 336 base pairs

45 Strandedness: double

Topology: linear

Source: human cDNA

Immediate experimental source: E.coli LC 137/pPLMu.TGF-β3(44/45)β2

50 Features: from 1 to 336 coding region for TGF-β3(44/45)β2 hybrid

55

EP 0 542 679 A1

5	GCT TTG GAC ACC AAT TAC TGC TTC CGC AAC TTG GAG GAG Ala Leu Asp Thr Asn Tyr Cys Phe Arg Asn Leu Glu Glu	39
	5 10	
10	AAC TGC TGT GTG CGC CCC CTC TAC ATT GAC TTC CGA CAG Asn Cys Cys Val Arg Pro Leu Tyr Ile Asp Phe Arg Gln	78
	15 20 25	
15	GAT CTG GGC TGG AAG TGG GTC CAT GAA CCT AAG GGC TAC Asp Leu Gly Trp Lys Trp Val His Glu Pro Lys Gly Tyr	117
	30 35	
20	TAT GCC AAC TTC TGT GCT GGA GCA TGC CCG TAT TTA TGG Tyr Ala Asn Phe Cys Ala Gly Ala Cys Pro Tyr Leu Trp	156
	40 45 50	
25	AGT TCA GAC ACT CAG CAC AGC AGG GTC CTG AGC TTA TAT Ser Ser Asp Thr Gln His Ser Arg Val Leu Ser Leu Tyr	195
	55 60 65	
30	AAT ACC ATA AAT CCA GAA GCA TCT GCT TCT CCT TGC TGC Asn Thr Ile Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys	234
	70 75	
35	GTG TCC CAA GAT TTA GAA CCT CTA ACC ATT CTC TAC TAC Val Ser Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr	273
40	80 85 90	
45	ATT GGC AAA ACA CCC AAG ATT GAA CAG CTT TCT AAT ATG Ile Gly Lys Thr Pro Lys Ile Glu Gln Leu Ser Asn Met	312
	95 100	
50	ATT GTA AAG TCT TGC AAA TGC AGC Ile Val Lys Ser Cys Lys Cys Ser	336
	105 110	
55		

SEQ ID NO. 10

Sequence Type: Nucleotide

Sequence length: 29 bases

Strandedness: single

Topology: linear

Source: synthetic oligonucleotide

Features: Oligo No. 1; TGF- $\beta$ 1 sense strand, includes NcoI site and represents the 5' end of the sequence encoding the mature peptide.

TCCCGGCACA CCATGGCCCT GGACACCAA 29

SEQ ID NO. 11

Sequence Type: Nucleotide

Sequence length: 27 bases

Strandedness: single

Topology: linear

Source: synthetic oligonucleotide

Features: Oligo No. 2; TGF- $\beta$ 1 antisense strand, includes SalI site and represents the 3' end of the sequence encoding the mature peptide.

CGGGGCGTCG ACTCAGCTGC ACTTGCA 27

SEQ ID NO. 12

Sequence Type: Nucleotide

Sequence length: 30 bases

Strandedness: single

Topology: linear

Source: synthetic oligonucleotide

5 Features: Oligo No. 3; TGF- $\beta$ 2 sense strand, includes NcoI site and represents the 5' end of the sequence encoding the mature peptide.

10 CGGCGGAAGA CCATGGCTTT GGATGCGGCC 30

15 SEQ ID NO. 13

Sequence Type: Nucleotide

Sequence length: 27 bases

20 Strandedness: single

Topology: linear

Source: synthetic oligonucleotide

25 Features: Oligo No. 4; TGF- $\beta$ 2 antisense strand, includes SalI site and represents the 3' end of the sequence encoding the mature peptide.

30 TTTCCAGTCG ACTTAGCTGC ATTGCA 27

35 SEQ ID NO. 14

Sequence Type: Nucleotide

Sequence length: 29 bases

40 Strandedness: single

Topology: linear

Source: synthetic oligonucleotide

45 Features: Oligo No. 5; TGF- $\beta$ 3 sense strand, includes NcoI site and represents the 5' end of the sequence encoding the mature peptide.

50 CAGAGGAAGA CCATGGCTTT GGACACCAA 29

55

SEQ ID NO. 15

Sequence Type: Nucleotide

Sequence length: 27 bases

Strandedness: single

Topology: linear

Source: synthetic oligonucleotide

Features: Oligo No. 6; TGF- $\beta$ 3 antisense strand, includes SalI site and represents the 3' end of the sequence encoding the mature peptide.

GCACGTGTCG ACTCAGCTAC ATTTACA 27

SEQ ID NO.16

Sequence Type: Nucleotide

Sequence length: 21 bases

Strandedness: single

Topology: linear

Source: synthetic oligonucleotide

Features: Oligo No. 7; TGF- $\beta$ 1 sense strand, nucleotides 111 - 131.

GGGCTACCAT GCCAACTTCT G 21

SEQ ID NO. 17

Sequence Type: Nucleotide

Sequence length: 21 bases

Strandedness: single

Topology: linear

Source: synthetic oligonucleotide

Features: Oligo No. 8; TGF- $\beta$ 1 antisense strand, nucleotides 111 - 131.

CAGAAGTTGG CATGGTAGCC C 21

SEQ ID NO. 18

Sequence Type: Nucleotide

5 Sequence length: 21 bases

Strandedness: single

Topology: linear

10 Source: synthetic oligonucleotide

Features: Oligo No. 9; TGF- $\beta$ 3 sense strand, nucleotides 111 - 131.

15 GGGCTACTAT GCCAACTTCT G

21

20 SEQ ID NO. 19

Sequence Type: Nucleotide

Sequence length: 21 bases

25 Strandedness: single

Topology: linear

Source: synthetic oligonucleotide

Features: Oligo No. 10; TGF- $\beta$ 3 antisense strand, nucleotides 111 - 131.

30 CAGAAGTTGG CATAGTAGCC C

21

35 SEQ ID NO. 20

Sequence Type: Nucleotide

40 Sequence length: 21 bases

Strandedness: single

Topology: linear

45 Source: synthetic oligonucleotide

Features: Oligo No. 11; TGF- $\beta$ 2 sense strand, nucleotides 111 - 131.

50 AGGGTACAAT GCCAACTTCT G

21

55

SEQ ID NO. 21

Sequence Type: Nucleotide

Sequence length: 21 base

Strandedness: single

Topology: linear

Source: synthetic oligonucleotide

Features: Oligo No. 12; TGF- $\beta$ 2 antisense strand, nucleotides 111 - 131.

CAGAAGTTGG CATTGTACCC T

21

SEQ ID NO. 22

Sequence Type: Nucleotide

Sequence length: 21 bases

Strandedness: single

Topology: linear

Source: synthetic oligonucleotide

Features: Oligo No. 13; TGF- $\beta$ 1 sense strand, nucleotides 48 - 68.

CGTGCGGCAG CTGTACATTG A

21

SEQ ID NO. 23

Sequence Type: Nucleotide

Sequence length: 21 bases

Strandedness: single

Topology: linear

Source: synthetic oligonucleotide

Features: Oligo No. 14; TGF- $\beta$ 1 antisense strand, nucleotides 68 - 48.

TCAATGTACA GCTGCCGCAC G

21

SEQ ID NO. 24

Sequence Type: Nucleotide

Sequence length: 21 bases

Strandedness: single

Topology: linear

Source: synthetic oligonucleotide

Features: Oligo No. 15; TGF- $\beta$ 2 sense strand, nucleotides 48 - 68.

CCTACGTCCA CTTTACATTG A

SEQ ID NO. 25

Sequence Type: Nucleotide

Sequence length: 21 bases

Strandedness: single

Topology: linear

Source: synthetic oligonucleotide

Features: Oligo No. 16; TGF- $\beta$ 2 antisense strand, nucleotides 68 - 48.

TCAATGTAAA GTGGACGTAG G

21

SEQ ID NO. 26

Sequence Type: Nucleotide

Sequence length: 21 bases

Strandedness: single

Topology: linear

Source: synthetic oligonucleotide

Features: Oligo No. 17; TGF- $\beta$ 3 sense strand, nucleotides 48 - 68.

TGTGCGCCCC CTCTACATTG A

21

SEQ ID NO. 27

Sequence Type: Nucleotide

Sequence length: 21 bases

Strandedness: single

Topology: linear

Source: synthetic oligonucleotide

Features: Oligo No. 18; TGF- $\beta$ 3 antisense strand, nucleotides 68 - 48.

TCAATGTAGA GGGGGCGCAC A 21

SEQ ID NO. 28

Sequence Type: Nucleotide

Sequence length: 26 bases

Strandedness: single

Topology: linear

Source: synthetic oligonucleotide

Features: Oligo No. 19; TGF- $\beta$ 1 sense strand, nucleotides 142-167.

TGCCCCTACA TTTGGAGCCT GGACAC 26

SEQ ID NO. 29

Sequence Type: Nucleotide

Sequence length: 26 bases

Strandedness: single

Topology: linear

Source: synthetic oligonucleotide

Features: Oligo No. 20; TGF- $\beta$ 1 antisense strand, nucleotides 167-142.

GTGTCCAGGC TCCAAATGTA GGGGCA 26

SEQ ID NO. 30

Sequence Type: Nucleotide

Sequence length: 26 bases

Strandedness: single

Topology: linear

Source: synthetic oligonucleotide

Features: Oligo No. 21; TGF- $\beta$ 2 sense strand, nucleotides 142-167.

TGCCCCGTATT TATGGAGTTC AGACAC 26

SEQ ID NO. 31

Sequence Type: Nucleotide

Sequence length: 26 bases

Strandedness: single

Topology: linear

Source: synthetic oligonucleotide

Features: Oligo No. 22; TGF- $\beta$ 2 antisense strand, nucleotides 167-142.

GTGTCTGAAC TCCATAAATA CGGGCA 26

SEQ ID NO. 32

Sequence Type: Nucleotide

Sequence length: 26 bases

Strandedness: single

Topology: linear

Source: synthetic oligonucleotide

Features: Oligo No. 23; TGF- $\beta$ 3 sense strand, nucleotides 142-167.

TGCCCATACC TCTGTAGTGC AGACAC 26

SEQ ID NO. 33

Sequence Type: Nucleotide

Sequence length: 26 bases

Strandedness: single

Topology: linear

Source: synthetic oligonucleotide

Features: Oligo No. 24; TGF- $\beta$ 3 antisense strand, nucleotides 167-142.

GTGTCTGAAC TGC GGAGGTA TGGTCA 26

SEQ ID NO. 34

Sequence Type: Nucleotide

Sequence length: 21 bases

Strandedness: single

Topology: linear

Source: synthetic oligonucleotide

Features: Oligo No. 25; TGF- $\beta$ 1 sense strand, nucleotides 217-237.

TCGGCGGCGC CGTGCTGCGT G 21

SEQ ID NO. 35

Sequence Type: Nucleotide

Sequence length: 21 bases

Strandedness: single

Topology: linear

Source: synthetic oligonucleotide

Features: Oligo No. 26; TGF- $\beta$ 1 antisense strand, nucleotides 237-217.

CACGCAGCAC GGCGCCGCCG A 21

SEQ ID NO. 36

Sequence Type: Nucleotide

Sequence length: 21 bases

Strandedness: single

Topology: linear

Source: synthetic oligonucleotide

Features: Oligo No. 27; TGF- $\beta$ 2 sense strand, nucleotides 217-237.

TCTGCTTCTC CTTGCTGCGT G 21

SEQ ID NO. 37

Sequence Type: Nucleotide

Sequence length: 21 bases

Strandedness: single

Topology: linear

Source: synthetic oligonucleotide

Features: Oligo No. 28; TGF- $\beta$ 2 antisense strand, nucleotides 237-217.

CACGCAGCAA GGAGAAGCAG A 21

SEQ ID NO. 38

Sequence Type: Nucleotide

Sequence length: 21 bases

Strandedness: single

Topology: linear

Source: synthetic oligonucleotide

Features: Oligo No. 29; TGF- $\beta$ 3 sense strand, nucleotides 217-237.

TCTGCCTCGC CTTGCTGCGT G 21

SEQ ID NO. 39

Sequence Type: Nucleotide

Sequence length: 21 bases

Strandedness: single

Topology: linear

Source: synthetic oligonucleotide

Features: Oligo No. 30; TGF- $\beta$ 3 antisense strand, nucleotides 237-217.

CACGCAGCAA GGCGAGGCAG A 21

SEQ ID NO. 40

Sequence Type: Nucleotide

Sequence length: 21 bases

Strandedness: single

Topology: linear

Source: synthetic oligonucleotide

Features: Oligo No. 31; TGF- $\beta$ 1 sense strand, nucleotides 252-272.

GCCGCTGCCC ATCGTGTACT A 21

SEQ ID NO. 41

Sequence Type: Nucleotide

Sequence length: 21 bases

Strandedness: single

Topology: linear

Source: synthetic oligonucleotide

Features: Oligo No. 32; TGF- $\beta$ 1 antisense strand, nucleotides 272-252.

TAGTACACGA TGGGCAGCGG C 21

SEQ ID NO. 42

Sequence Type: Nucleotide

5 Sequence length: 21 bases

Strandedness: single

Topology: linear

10 Source: synthetic oligonucleotide

Features: Oligo No. 33; TGF- $\beta$ 2 sense strand, nucleotides 252-272.

15 ACCTCTAACC ATTCTCTACT A 21

SEQ ID NO. 43

20 Sequence Type: Nucleotide

Sequence length: 21 bases

Strandedness: single

25 Topology: linear

Source: synthetic oligonucleotide

Features: Oligo No. 34; TGF- $\beta$ 2 antisense strand, nucleotides 272-252.

30 TAGTAGAGAA TGGTTAGAGG T 21

SEQ ID NO. 44

40 Sequence Type: Nucleotide

Sequence length: 21 bases

Strandedness: single

45 Topology: linear

Source: synthetic oligonucleotide

Features: Oligo No. 35; TGF- $\beta$ 3 sense strand, nucleotides 252-272.

50 GCCCTGACCA TCCTGTACT A 21

55

SEQ ID NO. 45

5 Sequence Type: Nucleotide  
 Sequence length: 21 bases  
 Strandedness: single  
 Topology: linear  
 10 Source: synthetic oligonucleotide  
 Features: Oligo No. 36; TGF- $\beta$ 3 antisense strand, nucleotides 272-252.

15 TAGTACAGGA TGGTCAGGGG C 21

SEQ ID NO. 46

20 Sequence Type: Nucleotide  
 Sequence length: 34 bases  
 Strandedness: single  
 25 Topology: linear  
 Source: synthetic oligonucleotide  
 Features: Oligonucleotide I-1, encodes part of the invertase signal sequence

30 AATTCATGCT TTTGCAAGCT TTCCTTTTCC TTTT 34

SEQ ID NO. 47

35 Sequence Type: Nucleotide  
 Sequence length: 35 bases  
 40 Strandedness: single  
 Topology: linear  
 Source: synthetic oligonucleotide  
 45 Features: Oligonucleotide I-2, complementary to Oligonucleotide I-1

50 CAGCCAAAAG GAAAAGGAAA GCTTGCAAAA GCATG 35

55

SEQ ID NO. 48

Sequence Type: Nucleotide

Sequence length: 38 bases

Strandedness: single

Topology: linear

Source: synthetic oligonucleotide

Features: Oligonucleotide I-3, encodes part of the invertase signal sequence

GGCTGGTTTT GCAGCCAAAA TATCTGCATC TTAGCGTC  
38

SEQ ID NO. 49

Sequence Type: Nucleotide

Sequence length: 37 bases

Strandedness: single

Topology: linear

Source: synthetic oligonucleotide

Features: Oligonucleotide I-4, complementary to Oligonucleotide I-3

TCGAGACGCT AAGATGCAGA TATTTTGGCT GCAAAAC  
37

FD4.4/BO

Claims

1. A hybrid TGF- $\beta$  molecule consisting of two or more parts, said parts consisting of contiguous stretches of 6 or more amino acids of a sequence which occurs in mature TGF- $\beta$  isoforms.
2. A hybrid TGF- $\beta$  molecule according to claim 1 consisting of 2, 3, 4, 5 or 6 parts.
3. A hybrid TGF- $\beta$  molecule according to claim 1 consisting of two parts.
4. A hybrid TGF- $\beta$  molecule according to claim 3 consisting of parts of the TGF- $\beta$  isoforms human TGF- $\beta$ 1, human TGF- $\beta$ 2 and human TGF- $\beta$ 3 with the amino acid sequences depicted the Sequence Listing under SEQ ID NO. 1 to 3.
5. A hybrid TGF- $\beta$  molecule according to claim 1 having a hinge point between parts derived from different parent TGF- $\beta$  isoforms selected from the group of hinge points between amino acids 44 and 45, 56 and 57, 79 and 80, 90 and 91, and 22 and 23.

6. A hybrid TGF- $\beta$  molecule according to claim 1 selected from the group consisting of the hybrids consisting of a N-terminal part of TGF- $\beta$ 1 and a C-terminal part of TGF- $\beta$ 2, a N-terminal part of TGF- $\beta$ 2 and a C-terminal part of TGF- $\beta$ 1, a N-terminal part of TGF- $\beta$ 1 and a C-terminal part of TGF- $\beta$ 3, a N-terminal part of TGF- $\beta$ 3 and a C-terminal part of TGF- $\beta$ 1, a N-terminal part of TGF- $\beta$ 2 and a C-terminal part of TGF- $\beta$ 3, and a N-terminal part of TGF- $\beta$ 3 and a C-terminal part of TGF- $\beta$ 2.
7. A hybrid TGF- $\beta$  molecule according to claim 1 selected from the group consisting of the hybrids TGF- $\beta$ 1(44/45) $\beta$ 2, TGF- $\beta$ 2(44/45) $\beta$ 1, TGF- $\beta$ 1(44/45) $\beta$ 3, TGF- $\beta$ 3(44/45) $\beta$ 1, TGF- $\beta$ 2(44/45) $\beta$ 3, TGF- $\beta$ 3(44/45) $\beta$ 2, TGF- $\beta$ 1(56/57) $\beta$ 2, TGF- $\beta$ 2(56/57) $\beta$ 1, TGF- $\beta$ 1(56/57) $\beta$ 3, TGF- $\beta$ 3(56/57) $\beta$ 1, TGF- $\beta$ 2(56/57) $\beta$ 3, TGF- $\beta$ 3(56/57) $\beta$ 2, TGF- $\beta$ 1(79/80) $\beta$ 2, TGF- $\beta$ 2(79/80) $\beta$ 1, TGF- $\beta$ 1(79/80) $\beta$ 3, TGF- $\beta$ 3(79/80) $\beta$ 1, TGF- $\beta$ 3(79/80) $\beta$ 2, TGF- $\beta$ 2(79/80) $\beta$ 3, TGF- $\beta$ 1(90/91) $\beta$ 2, TGF- $\beta$ 2(90/91) $\beta$ 1, TGF- $\beta$ 1(90/91) $\beta$ 3, TGF- $\beta$ 3(90/91) $\beta$ 1, TGF- $\beta$ 3(90/91) $\beta$ 2, TGF- $\beta$ 2(90/91) $\beta$ 3, TGF- $\beta$ 1(22/23) $\beta$ 2, TGF- $\beta$ 2(22/23) $\beta$ 1, TGF- $\beta$ 1(22/23) $\beta$ 3, TGF- $\beta$ 3(22/23) $\beta$ 1, TGF- $\beta$ 3(22/23) $\beta$ 2, and TGF- $\beta$ 2(22/23) $\beta$ 3.
8. A hybrid TGF- $\beta$  molecule according to claim 1 selected from the group consisting of the hybrids TGF- $\beta$ 1(44/45) $\beta$ 2, TGF- $\beta$ 2(44/45) $\beta$ 1, TGF- $\beta$ 1(44/45) $\beta$ 3, TGF- $\beta$ 3(44/45) $\beta$ 1, and TGF- $\beta$ 2(44/45) $\beta$ 3, TGF- $\beta$ 3(44/45) $\beta$ 2 depicted in the sequence listing under SEQ ID NOs. 4 to 9.
9. The hybrid TGF- $\beta$  molecule according to claim 1 which is TGF- $\beta$ 3(44/45) $\beta$ 2 depicted in the sequence listing under SEQ ID NO. 9.
10. A recombinant DNA molecule encoding a hybrid TGF- $\beta$  molecule according to claim 1.
11. A recombinant DNA molecule according to claim 10 which is an expression vector for the preparation of a hybrid TGF- $\beta$  molecule.
12. A method for the preparation of a DNA molecule according to claim 10.
13. A host transformed with a DNA molecule according to claim 10.
14. A method for the preparation of a hybrid TGF- $\beta$  molecule according to claim 1.
15. A pharmaceutical composition comprising a hybrid TGF- $\beta$  molecule according to claim 1.

EP 0 542 679 A1



European Patent  
Office

# EUROPEAN SEARCH REPORT

Application Number

EP 92 81 0845

DOCUMENTS CONSIDERED TO BE RELEVANT			
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (Int. Cl. 5)
A	EP-A-0 374 044 (ONCOGENE LIMITED PARTNERSHIP) * page 5, line 5 - line 33 *	1-15	C12N15/12 C12N15/62 A61K37/02 C12N1/21 /(C12N1/21, C12R1:865)
D,A	EP-A-0 433 225 (CIBA-GEIGY A.G.) * the whole document *	1-15	
A	EP-A-0 376 785 (ONCOGENE LIMITED PARTNERSHIP) * page 19, line 45 - page 21, line 21; figure 1C *	1-15	
D,A	EP-A-0 267 463 (ONCOGENE SCIENCE, INC.) * page 41, line 54 - page 42, line 5; claims; figure 31 *	1-15	
P,X	PROC. NATL. ACAD. SCI. U. S. A. vol. 89, no. 14, 15 July 1992, pages 6290 - 6294 QIAN, S.W. ET AL. 'Identification of a structural domain that distinguishes the actions of the type 1 and 2 isoforms of transforming growth factor beta on endothelial cells' * the whole document *	1-2,4, 10-14	
			TECHNICAL FIELDS SEARCHED (Int. Cl. 5)
			C07K C12N A61K
The present search report has been drawn up for all claims			
Place of search THE HAGUE		Date of completion of the search 01 FEBRUARY 1993	Examiner ANDRES S.M.
CATEGORY OF CITED DOCUMENTS		T : theory or principle underlying the invention E : earlier patent document, but published on, or after the filing date D : document cited in the application L : document cited for other reasons A : technological background O : non-written disclosure P : intermediate document & : member of the same patent family, corresponding document	
X : particularly relevant if taken alone Y : particularly relevant if combined with another document of the same category			

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